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のガイダンスノート」を参照。

(54) Title: EXPRESSION SYSTEM OF ACTINOMYCETE-ORIGIN CYTOCHROME P-450 IN *ESCHERICHIA COLI*

(54) 発明の名称: 大腸菌における放線菌由来チトクローム P-450 遺伝子の発現系

(57) Abstract: It is intended to provide an expression system of cytochrome P-450 with the use of *Escherichia coli* as a host. An *E. coli* strain containing a ferredoxin gene originating in actinomycete, a ferredoxin gene foreign to *E. coli* and a ferredoxin reductase gene, which is useful in the progress of an effective reaction of adding monoatomic oxygen to an organic compound serving as a substrate, is provided.

(57) 要約: 宿主大腸菌を用いるチトクローム P-450 遺伝子の発現系の提供。放線菌由来のフェレドキシン遺伝子、ならびに大腸菌に対して異種のフェレドキシン遺伝子およびフェレドキシン還元酵素遺伝子を含む大腸菌が提供される、基質有機化合物の効果的な一原子酸素添加反応を進めるのに有用である。

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(54) **EXPRESSION SYSTEM OF ACTINOMYCETE-ORIGIN CYTOCHROME P-450 IN ESCHERICHIA COLI**

(57) This invention relates to a system for the expression of cytochrome P-450 gene in host *Escherichia coli*, and provides *Escherichia coli* which contains actinomycete ferredoxin gene and also ferredoxin gene and ferredoxin reductase gene which are xenogenic to *Es-*

cherichia coli.

Thus, this invention is useful for the promotion of effective single oxygen atom insertional reaction of a substrate organic compound.

Description

Technical Field

5 [0001] This invention relates to a system for the expression of actinomycete cytochrome P-450 genes in *Escherichia coli*.

Background Technology

10 [0002] Cytochrome P-450 enzymes (hereinafter referred to simply as "P-450s") which are encoded by cytochrome P-450 genes are a general name of a group of protoheme-containing proteins whose reduced form shows Soret band around 450 nm when bound to carbon monoxide. P-450s are bound to microsome in tissue of various kinds of animal or plant, or in fungi or yeasts, or to inner membrane of mitochondrion in tissue of some kind of animals. In certain kinds of bacteria and fungi, P-450s exist in soluble state.

15 [0003] P-450s show various types of substrate-specificity. Some P-450s have abnormally so wide substrate-specificity that they can react with various kinds of organic compounds as substrate. Some, on the other hand, have considerably strict substrate-specificity, and react only with comparatively limited kinds of organic compounds. P-450s also show excellent stereo- and/or regio-specificity to reaction site. With regard to concrete functions, P-450s are known to catalyze reactions such as hydroxylation, epoxidation, dealkylation and denitrification, of xenobiotics in a cell which
20 expresses said P-450s. For example, most of drugs which are administered to human are metabolized and inactivated in the body by various or specific action, such as hydroxylation, of P-450. In some cases, on the contrary, pharmacological effects of the drugs are improved, or subsidiary action is enhanced. P-450 is, therefore, medically very important from the viewpoint of the research of metabolism of medicine or the development of prodrugs.

25 [0004] Thus, P-450s which have drug-metabolizing functions for higher organisms including human have been studied from every angle for long years. Although these enzymes are obtained from microsome fractions of liver of higher organisms, it is difficult to purify these enzymes into single isozyme. On this account, there has been developed a technology to express functionally a gene which encodes single isozyme in a host such as *Escherichia coli* or yeast, and to thus conveniently investigate the metabolic role of the enzyme.

30 [0005] P-450s of higher organisms which have such drug-metabolizing functions as mentioned above have never been successfully applied to material production on industrial scale. P-450s of higher organisms, when functionally expressed in a host such as *Escherichia coli* or yeast, show only low productivity as compared with P-450s of bacteria, and also cause various side reactions. For these reasons, P-450s of higher organisms have been used only restrictively.

35 [0006] In the case of P-450 originated from microorganisms such as fungi and bacteria, on the other hand, some kinds of P-450s are known to serve for the production of industrially useful materials. Some of such kinds of P-450s have actually been utilized for industrial production of useful medicine. Typical example is the production of pravastatin, a medicine to remedy hyperlipidemia, by means of the hydroxylation at 6 β -position of compactin with *Streptomyces carbophilus*, a species of actinomycete (Watanabe et al., Gene, 163 (1995) 81-85, Japanese Patent Application Laid-Open (Kokai) Publication No. Hei 6 (1994)-70780). There has also been put into practice a method by which to produce active vitamin D₃ by means of the hydroxylation at 1 α - and 25-positions of vitamin D₃ with use of *Pseudonocardia autotrophica*, a species of actinomycete.
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[0007] Such microbial conversion of drugs with use of actinomycete cytochrome P-450 enzymes as mentioned above have been carried out with use of culture liquids or cells of actinomycetes which express said enzymes. There have also been used culture liquids wherein genes which encode actinomycete P-450s have been introduced into *Streptomyces lividans*, that is also a species of actinomycete and that is suitable as a host, to express the enzymatic activity.
45 The microbial conversion of substrate compounds with the actinomycete strains which have such genes as mentioned above takes considerable time for the cultivation of the strains and for the conversion of substrate compounds into desired products. Furthermore, some enzymes need consideration on expression-inducible conditions under which to increase the amount of enzyme expressed. Moreover, some species of actinomycetes which are to be used for the conversion have, in themselves, a system for metabolizing or degrading substrate or desired product, which causes
50 the formation of by-products or the reduction of substrate or desired product, and thus decreases the productivity of desired product.

[0008] There is also a report of experiment wherein, after the example of functionally expressing a gene which encodes single isozyme of the above-mentioned higher organism-originated P-450s in a host of microorganism such as *Escherichia coli*, CYP105D1 gene which is a *Streptomyces griseus* originated cytochrome P-450 gene was functionally expressed in *Escherichia coli* (Taylor et al., Biochemical and Biophysical Research Communications (1999) 263: 838-842). It seems that, in this expression system, some suitable electron donor for the P-450 in periplasm of *Escherichia coli* hydroxylates hydrocarbons in cooperation with the P-450 (Kaderbhai et al., Applied and Environmental Microbiology, 67 (2001) 2136-2138). Such a P-450 gene-expressing system has a merit that *Escherichia coli* as a host
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needs less time for cultivation as compared with actinomycetes or the like.

Disclosure of Invention

[0009] The above-mentioned system for the conversion of organic compounds with microorganisms which have P-450s is intended to be used, for instance, for the application to biocatalyst or for the research of drug metabolism. In consideration of application to biocatalyst, in particular, more efficient bioconversion would be demanded. In order to achieve the efficient screening of industrially important and desired actinomycete P-450 enzymes, there would be needed a suitable gene library as an object of robotized enzyme-assaying operation or other convenient and rapid enzyme-assaying operation in high throughput screening or the like. Concretely, there is demanded a library which has actinomycete-originated different cytochrome P-450 genes (actinomycete cytochrome P-450-expression library) and wherein microorganism, preferably handy and quick-growing microorganism, is used as a host in which each constituent clone is capable of expression.

[0010] In order to attain the above-mentioned objective, it would be useful to use, as a host, *Escherichia coli* which, at least, needs comparatively short time for cultivation, and which is considered to have only a few systems for the metabolism or degradation of substrate compounds or products from said substrate compounds. It has been confirmed, however, that only introducing an actinomycete P-450 gene into a host *Escherichia coli* and cultivating the same, as in the above-mentioned Taylor *et al.* wherein *Escherichia coli* is used as a host, does not achieve the functional expression of most of various kinds of P-450 genes which are originated from other species of actinomycete (or, in other words, enzymatic activity of P-450 is not shown as expected). Thus, the inventors of the present invention have studied how to construct a system which is capable of functionally expressing actinomycete-originated various kinds of P-450 genes surely and with high enzymatic activity. As a result, they have found out that, when a certain electron transport system originated from microorganism which is xenogenic to *Escherichia coli* is introduced together with P-450 gene and is then allowed to co-express, the P-450 gene originated from various species of actinomycete is functionally expressed.

[0011] Based on such a finding as mentioned above, this invention provides a system for the expression of actinomycete cytochrome P-450 genes in host *Escherichia coli*, wherein said *Escherichia coli* supports a recombinant DNA molecule which comprises xenogenic microorganism-originated ferredoxin gene, ferredoxin reductase gene and said cytochrome P-450 gene in operable state.

[0012] Such an expression system as explained above is capable of the expression of such a gene as mentioned in the above Taylor *et al.* which encodes actinomycete cytochrome P-450, and which is incapable of conjugating native electron transport system of *Escherichia coli*. In other words, the expression system of this invention achieves expected enzymatic activity of P-450 whether P-450 gene may conjugate native electron transport system of *Escherichia coli* or not. Thus, the term "functionally express" in this specification means that, a gene of interest expresses protein, which is encoded by the gene, in an active form.

[0013] In the following, this invention is explained in more detail.

[0014] Host *Escherichia coli* means certain kinds of *Escherichia coli* which are usable for the propagation of vectors such as plasmids and phages and of inserted genes. Any species of host will do if only, in a recombinant DNA experiment with use of host-vector system, a vector with an exogenous DNA fragment is capable of replication after transformation. As a host for said host-vector system, *Escherichia coli* on the market would be conveniently utilized.

[0015] Actinomycete cytochrome P-450 genes in this invention include P-450 genes originated from any genus of bacteria that belong to order *Actinomycetales* if only the bacteria have P-450 genes which serve to achieve the objective of this invention in some form or other (e.g., on chromosome or plasmid). Thus, cytochrome P-450 genes include all that encodes protein mentioned above which has such activity as to catalyze single oxygen atom insertional reaction in accordance with this invention. Although not restrictive, examples of P-450 genes which are intended to be incorporated into the expression system of this invention include those which have the above-mentioned function, at least a part of whose DNA sequences have been determined, and each of whose sequence information is available from gene data base (EMBL and GenBank), concretely, those which are originated from the following species of actinomycete and which encode protein having the above-mentioned activity, or those which have functions of cytochrome P-450 as mentioned below.

Actinomycete	Function of cytochrome P-450
<i>Amycolatopsis orientalis</i>	Unknown
<i>Actinomadura verrucosospora</i>	Biosynthesis of vercopeptin
<i>Amycolata autotrophica</i>	Unknown
<i>Amycolatopsis mediterranei</i>	Biosynthesis of rifamycin

(continued)

	Actinomycete	Function of cytochrome P-450
5	<i>Amycolatopsis mediterranei</i>	Biosynthesis of balhimycin
	<i>Kitasatospora griseospola</i>	Biosynthesis of terpentecin
	<i>Micromonospora griseorubida</i>	Biosynthesis of mycinamicin
	<i>Micromonospora inyoensis</i>	Unknown
	<i>Microtetraspora recticatena</i>	Hydroxylation of compactin
10	<i>Mycobacterium smegmatis</i> mc2155	Degradation of piperidine and pyrrolidine
	<i>Mycobacterium</i> sp. FM10	Unknown
	<i>Mycobacterium tuberculosis</i> H37Rv	22 P-450 genes in whole genome (function unknown)
	<i>Myxococcus xanthus</i>	Polyketide antibiotic TA
15	<i>Pseudonocardia autotrophica</i> (old name: <i>Amycolata autotrophica</i>)	Hydroxylation of vitamin D ₃
	<i>Rhodococcus erythropolis</i>	Degradation of thiocarbamate herbicide
	<i>Rhodococcus fascians</i> (D 188)	Synthesis of phytophysiologically active substance
	<i>Rhodococcus ruber</i>	Degradation of ethyl- <i>tert</i> -butyl ether
20	<i>Saccharopolyspora erythraea</i>	Hydroxylation of erythromycin
	<i>Streptoalloteichus hindustanus</i>	Unknown
	<i>Streptomyces acidiscabies</i>	Biosynthesis of thaxtomin A
	<i>Streptomyces albus</i>	Unknown
	<i>Streptomyces ansochromogenes</i>	Biosynthesis of nikkomycin
25	<i>Streptomyces antibioticus</i>	Biosynthesis of oleandomycin
	<i>Streptomyces antibioticus</i>	Biosynthesis of simocyclinone
	<i>Streptomyces aureofaciens</i> Re n 71	Unknown
	<i>Streptomyces avermitilis</i>	Formation of furan ring of avermectin
30	<i>Streptomyces avermitilis</i>	Biosynthesis of oligomycin
	<i>Streptomyces avermitilis</i>	Biosynthesis of polyketide-4
	<i>Streptomyces avermitilis</i>	Biosynthesis of polyketide-9
	<i>Streptomyces avermitilis</i>	Biosynthesis of other type polyketide
35	<i>Streptomyces avermitilis</i>	Biosynthesis of polyene macrolide
	<i>Streptomyces avermitilis</i>	Biosynthesis of peptide-7
	<i>Streptomyces carbophilus</i>	Hydroxylation of compactin
	<i>Streptomyces clavuligerus</i>	Biosynthesis of clavulanic acid
40	<i>Streptomyces coelicolor</i> A3(2)	18 P-450 genes in whole genome (function unknown)
	<i>Streptomyces fluvus</i>	Hydroxylation of compactin
	<i>Streptomyces fradiae</i>	Biosynthesis of tylosin
	<i>Streptomyces glaucescens</i>	Unknown
45	<i>Streptomyces griseolus</i>	Degradation of sulfonyleurea herbicide
	<i>Streptomyces griseus</i>	Unknown
	<i>Streptomyces hygroscopicus</i>	Biosynthesis of rapamycin
	<i>Streptomyces hygroscopicus</i> var. <i>ascomyceticus</i>	Biosynthesis of FK520
50	<i>Streptomyces lavendulae</i>	Biosynthesis of mitomycin
	<i>Streptomyces la vendulae</i>	Biosynthesis of complestatin
	<i>Streptomyces lividans</i>	Unknown
	<i>Streptomyces maritimus</i>	Biosynthesis of enterocin
	<i>Streptomyces natalensis</i>	Biosynthesis of pimaricin
55	<i>Streptomyces nodosus</i>	Biosynthesis of amphotericin
	<i>Streptomycesnogalater</i>	Biosynthesis of nogalamycin
	<i>Streptomyces noursei</i>	Biosynthesis of nystatin

(continued)

Actinomycete	Function of cytochrome P-450
<i>Streptomyces peucetius</i>	Hydroxylation of daunomycin
<i>Streptomyces peucetius</i> subsp. <i>caesius</i>	Hydroxylation of daunomycin
<i>Streptomyces rishiriensis</i> strain DSM 40489	Biosynthesis of coumermycin A1
<i>Streptomyces sclerotialus</i>	Unknown
<i>Streptomyces</i> sp.	Hydroxylation of FK-506
<i>Streptomyces</i> sp.	Unknown
<i>Streptomyces spheroids</i>	Biosynthesis of novobiocin
<i>Streptomyces tendae</i>	Biosynthesis of nikkomycin
<i>Streptomyces thermotolerans</i>	Epoxidation of carbomycin
<i>Streptomyces venezuelae</i>	Biosynthesis of pikromycin, methymycin

[0016] The following actinomycete P-450 are also included as usable in this invention. Each of the following literatures gives guidance how to prepare gene which encodes each enzyme.

Compactin-hydroxylating enzyme originated from <i>Streptomyces carbophilus</i> (P-450 _{sca} -2)	Watanabe et al., Gene 163 (1995) 81-85 or Japanese Laid-Open (Kokai) Patent Publication No. Hei 6 (1994)-70780
<i>Microtetraspora recticatena</i>	Japanese Laid-Open (Kokai) Patent Publication No. 2001-286293
Vitamin D ₃ -hydroxylating enzyme originated from <i>Amycolata</i> sp.	Sasaki et al., Applied Microbiology and Biotechnology (1992) 38: 152-157

[0017] *Streptomyces roseochromogenes*-originated progesterone-hydroxylating enzyme (Berrie et al., Journal of Steroid Biochemistry & Molecular Biology 77 (2001) 87-96) can also be mentioned. Although gene sequence of this *Streptomyces roseochromogenes* is not mentioned in published literatures, function and biochemical properties of this P-450 enzyme have detailedly determined, and, on the basis of which information, it is easy to prepare gene which encodes said P-450 enzyme.

[0018] Cytochrome P-450-encoding genes (or P-450 genes) as mentioned in this invention include any gene so long as it can be isolated from total DNAs of the above-mentioned actinomycetes or can be amplified by PCR reaction, which is mentioned later, on the basis of information of nucleotide sequences of said total DNAs, and so long as it is capable of functional expression in the system of this invention for the expression of P-450 genes. Also included in P-450 genes of this invention are polynucleotides which are functionally equivalent to the above-mentioned genes (also called native gene), and which have activity to catalyze single oxygen atom insertional reaction against corresponding substrates in the expression system of this invention. It is guessed that complement base sequences of said equivalent polynucleotides hybridize with corresponding native genes under a certain hybridization condition, e.g., under stringent condition in $2 \times \text{SSC}$ (standard saline citrate) at 60°C, preferably in $0.5 \times \text{SSC}$ at 60°C, most desirably $0.2 \times \text{SSC}$ at 60°C. When each of the polynucleotides is lined up side by side with the corresponding native gene, there would be shown homology of 80 %, preferably 90 %, most desirably at least about 95 %. This "% homology" means percentage of nucleotide which is in common between two sequences when the two sequences are lined up side by side with each other in an optimum manner. [Thus, "% homology" = (number of coincident positions/total number of positions) x 100. This can be calculated with use of algorithm on the market. Such an algorithm is incorporated in NBLAST and XBLAST programs which are mentioned in Altschul et al., J. Mol. Biol. 215 (1990) 403-410.]

[0019] Ferredoxin gene which is incorporated in the expression system of this invention is a DNA molecule which is originated from microorganisms (or bacteria) which are xenogenic to host *Escherichia coli*. Ferredoxin gene generally encodes protein which functions as an electron transporter having a molecular weight of about 6,000 to 14,000. Ferredoxin gene may be originated from any bacteria except *Escherichia coli* so long as the bacteria participate in the functional expression of P-450 gene when co-expressed with the above-mentioned actinomycete P-450 gene and further with ferredoxin reductase gene which will be mentioned later. Concrete examples of said bacteria, although not restrictive, include actinomycete which may or may not be the same as mentioned above from which P-450 gene is originated.

[0020] Also usable is ferredoxin gene originated from bacteria, e.g., of genus *Pseudomonas*, which belong to different genus from that of actinomycete from which P-450 gene is originated. Examples of such a ferredoxin gene include putidaredoxin gene (also called *camB*) as mentioned in Peterson *et al.*, The Journal of Biological Chemistry, 265 (1990) 6066-6073.

[0021] When ferredoxin gene is originated from the same actinomycete from which P-450 gene is originated, P-450 gene and ferredoxin gene may sometimes constitute a gene cluster in which said P-450 gene and ferredoxin gene exist adjacent to each other on genomic DNA. In such a case, a DNA fragment which contains both of said genes may be used in the expression system of this invention. In the expression system of this invention, ferredoxin gene may exist with another ferredoxin. A preferable example of such a case is the use of ferredoxin gene originated from actinomycete in combination with the above-mentioned *camB* originated from *Pseudomonas putida*. Such a ferredoxin gene also includes functionally equivalent polynucleotide which can be specified in the same manner as in the above-mentioned P-450 gene.

[0022] Ferredoxin reductase gene which is incorporated in the expression system of this invention as an essential factor may be originated from bacteria which are xenogenic to host *Escherichia coli*, and which, under circumstances, may also be xenogenic to the origin of P-450 gene. Concretely, ferredoxin reductase gene originated from any bacteria is usable in this invention so long as the bacteria are capable of co-expression with the above-mentioned P-450 gene and with ferredoxin gene, and so long as the gene encodes ferredoxin reductase which shows the expected activity of P-450 enzyme, i.e., the product of said gene expression of P-450, or, in other words, which catalyzes single oxygen atom insertional reaction against substrate. Examples of such ferredoxin reductase gene, although non-restrictive, include ferredoxin reductase gene originated from *Streptomyces coelicolor* (hereinafter sometimes referred to as "fdr-1" or "fdr-2") and putidaredoxin reductase gene originated from the above-mentioned *Pseudomonas putida* (hereinafter referred to also as *camA*). Such a gene also includes functionally equivalent polynucleotide which can be specified in the same manner as in the above-mentioned P-450 gene.

[0023] In the expression system of this invention, the above-mentioned P-450 gene, ferredoxin gene and ferredoxin reductase gene are introduced in *Escherichia coli* in an operable state. The term "operable state" means that said genes are present in host in such a manner that all of the genes are capable of functional expression. In a typical example of such a state, all of the above-mentioned genes exist in a plasmid, which is capable of autonomous replication in *Escherichia coli*, together with autonomously replicating sequence, promoter sequence, terminator sequence and drug resistant gene, in a suitable order. Otherwise, all of said genes exist in chromosome of host *Escherichia coli* in such a manner that they are capable of functional expression via a chromosomal DNA integrative vector. The above-mentioned P-450 gene, ferredoxin gene and ferredoxin reductase gene may be arranged in any order in said plasmid. Usually, however, P-450 gene is preferably placed uppermost in the stream. When, in particular, P-450 gene and ferredoxin gene are used as a gene cluster fragment of the same origin, the following orders may be preferable: P-450 gene-ferredoxin gene-ferredoxin reductase gene; P-450 gene-ferredoxin gene-putidaredoxin reductase gene-putidaredoxin gene; or P-450 gene-putidaredoxin reductase gene-putidaredoxin gene.

[0024] Plasmid or vector which is usable in the above-mentioned expression system may be capable of stable autonomous replication in *Escherichia coli*, or may be an integrative vector which is capable of integrating chromosome of *Escherichia coli* with exogenous gene. Both can be available from those on the market, or by modification where necessary. Plasmids which have a strong promoter for gene transcription are conveniently used for the above-mentioned purpose. Examples of such plasmids include those on the market, such as pET11 and pUC18.

[0025] Thus provided actinomycete P-450 gene expression system of this invention is usable for the screening of P-450 enzymes which are suitable for the modification of various kinds of drugs or the bioconversion from precursor into desired drugs, or further for the manufacture of desired drugs from precursor.

Brief Explanation of Drawings

[0026]

Fig. 1 shows the structure of plasmid pMoxAB.

Fig. 2 shows the structure of plasmid pMoxAB-fdr1.

Fig. 3 shows the structure of plasmid pMoxAB-fdr2.

Fig. 4 shows the structure of plasmid pMoxAB-camAB.

Fig. 5 shows the structure of plasmid pT7NS-camAB.

Fig. 6 shows the structure of plasmid pCBM-camAB.

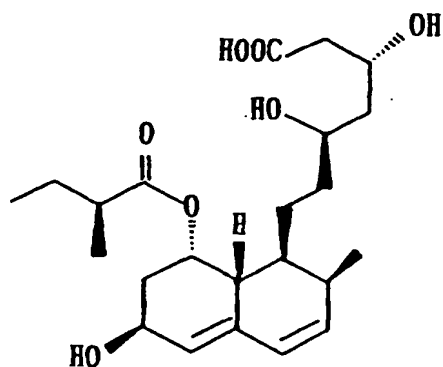
Fig. 7 shows the structure of plasmid pSC154A1-camAB.

Fig. 8 shows the structure of plasmid pDoxA1-camAB.

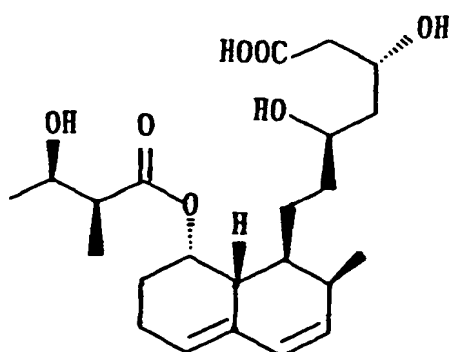
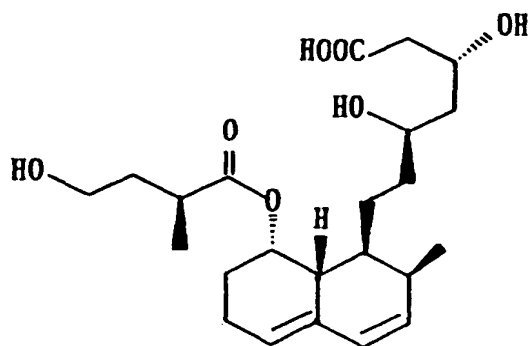
[0027] In the following, this invention is concretely explained with working examples.

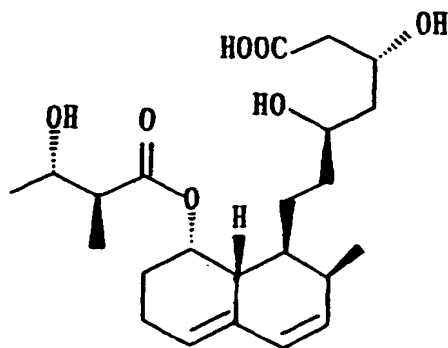
Best Mode for Working this Invention

[0028] This invention will be further explained with reference to examples of the construction of P-450 gene which forms pravastatin of the following formula:

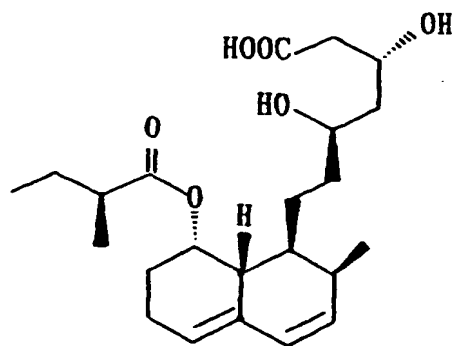


or a mixture (which is called "RT-5.8 substances" in this specification) of isomers thereof which have the following formulae:





by means of single oxygen atom insertional reaction of compactin of the following formula:



(or also existent as δ -lactone compound corresponding to the above formula) or a salt thereof.

[0029] Incidentally, pravastatin sodium is a clinically important medicine as an agent to cure hyperlipidemia.

[0030] Actinomycete which has an enzymatic activity to hydroxylate compactin (also called mevastatin) belongs to genus *Streptomyces* (Japanese Laid-Open (Kokai) Patent Publication Sho 57 (1982)-50894, Japanese Patent No. 2672551) or to genus *Microtetraspora*. As for the latter, which has been confirmed by the inventors of this invention, a DNA fragment which contains P-450 gene can be prepared by the following process.

Preparation of P-450 gene from *Microtetraspora recticatena* IFO 14525

[0031] Said gene can be obtained by polymerase chain reaction (PCR) with use of primers which have been designed in accordance with an amino acid sequence of the region which is known to keep amino acid sequence with a high probability among a family of lot of P-450 hydroxylation enzymes (J. Bacteriol. 172, 3335-3345 (1990)). For example, IFO 14525 strain is cultivated under certain cultivation conditions, and, then, thus obtained cells are crushed to give chromosomal DNA. Thus obtained chromosomal DNA is subjected to PCR reaction with use of primers which have been designed from amino acid sequences for oxygen-binding domain and heme-binding domain which exist in common with P-450 hydroxylation enzyme family. There is obtained a DNA fragment which has been amplified by the PCR reaction, on the basis of which a further PCR reaction is conducted, and, thus, there is obtained flanking regions of the DNA fragment which has been amplified by the first PCR reaction (in the downstream, there existed a gene which encoded ferredoxin). All of the above-mentioned manipulation can be carried out by any method that is known well in this art. Details of these sets of manipulation are mentioned in the specification of Japanese Patent Application No. 2001-47664 by the same applicant as that of the present application (the contents of said specification are incorporated into the present specification by citation). Sequence No. 1 in the sequence listing shows a nucleotide sequence (and amino acid sequences encoded) which includes adjacent region of thus obtained P-450 gene.

[0032] In the above-mentioned sequence, a continuous nucleotide sequence from base 313 to base 1533 corresponds to P-450 gene (*moxA*), and a continuous nucleotide sequence from base 1547 to base 1741 corresponds to ferredoxin gene (*moxB*).

Preparation of P-450 gene from *Streptomyces* sp. TM-6 or TM-7

[0033] From among a lot of microorganisms that belong to *Streptomyces* which were isolated from the soil in Japan, the applicant has identified the above-captioned TM-6 and TM-7 strains as microorganisms which are capable of biologically converting compactin as a substrate into pravastatin. Said strains were deposited on April 25, 2001, at the International Patent Organism Depository (IPOD) in the National Institute of Advanced Industrial Science and Technology (AIST) at Tsukuba Central 6, 1-1-1 Higashi, Tsukuba, Ibaraki, Japan, and thus have been received with Deposit Nos. FERM P-18311 and FERM P-18312.

[0034] Later, a demand was made on the above-mentioned IPOD, which is also an international depositary authority under the Budapest Treaty, for the transfer of these strains TM-6 and TM-7 to said international depositary authority under said Treaty, and, thus, these strains have been received with Deposit Nos. FERM BP-8002 and FERM BP-8003.

[0035] With regard to said TM-7 strain, a region of target gene was amplified by PCR in the same manner as in the above-mentioned IFO 14525, and, thus, the sequence of DNA fragment containing the target gene and its adjacent region was determined. The result is shown in Sequence No. 2. In this sequence, a continuous nucleotide sequence from base 544 to base 1758 corresponds to P-450 gene (*boxA*), and a continuous nucleotide sequence from base 1782 to base 1970 corresponds to ferredoxin gene (*boxB*). The manipulation to obtain these genes is mentioned detailedly in the specification of Japanese Patent Application No. 2001-166412 which has been filed by the applicant of the present application (the contents of said specification are incorporated into the present specification by citation).

[0036] When compared with the sequence of P-450 gene of *Streptomyces carbophilus* SANK 62585 strain (FERM BP-1145) which is mentioned, for instance, in Japanese Patent No. 2672551, the nucleotide sequence of the above-mentioned *boxA* was found to have a homology of about 75 %. With the above-mentioned *moxA*, the *boxA* has a homology of about 46 %. With hydroxylation enzyme gene of *Streptomyces lividans*, the *boxA* has a homology of about 75 %. Said *boxA* has a homology of about 46 % with a gene encoding pyridylhomothreonine monooxygenase which is an intermediate in the course of biosynthesis of nikkomycin by *Streptomyces tendae* Tji 901 strain.

[0037] On the basis of the above explanation or explanation in working examples mentioned below or, furthermore, on the basis of techniques which are known well in this art or of information in gene database, anyone skilled in the art would be able to obtain various kind of P-450 genes by means of firstly screening actinomycetes which are known (from type culture catalogue published by ATCC) with respect to bio-conversion of substrates for single oxygen atom insertion, then identifying strains having expected enzymatic activity, and thus conducting PCR operation as mentioned above. Hence, actinomycete cytochrome P-450 genes as called in this invention include not only known ones but also all that skilled persons could obtain.

[0038] The preparation of ferredoxin gene and ferredoxin reductase gene which are included in the expression system of this invention, and the construction of expression system by means of operable connection between these genes and P-450 genes, could be achieved quite easily by anyone skilled in the art in the same manner as in the above-mentioned P-450 genes, or in accordance with methods as mentioned in literatures (Sambrook *et al.*, Molecular Cloning, A Laboratory Manual, 3rd edition (2001), Cold Spring Harbor Laboratory Press, New York), and in the light of the methods in working examples as mentioned later.

[0039] Thus constructed expression system for P-450 genes is capable of functionally expressing P-450 genes under conditions where *Escherichia coli* is grown. When such an expression system is incubated under a suitable condition together with a substrate for enzyme as a product of P-450 gene (or when transformant as an expression system is cultivated), there is obtained a product wherein single oxygen atom has been inserted in substrate.

[0040] Cultivation is usually conducted on a medium which can be a nutritious medium for *Escherichia coli*, and which has no adverse effects on biological conversion of substrate. Such a medium is composed of suitable carbon source, nitrogen source, inorganic salt and natural organic nutriment. As said carbon source, there can be used glucose, fructose, glycerol, sorbitol and organic acids, either singly or in combination. The concentration of these carbon sources when used is suitably about 1 to 10 %, not particularly limited. As said nitrogen source, there can be employed one or two from ammonia, urea, ammonium sulfate, ammonium nitrate and ammonium acetate. As said inorganic salt, there can be used salts such as potassium dihydrogenphosphate, dipotassium hydrogenphosphate, magnesium sulfate, manganese sulfate and ferrous sulfate. As organic nutrient which has growth promoting effects on microorganism used, there can be used peptone, meat extract, yeast extract, corn steep liquor and casamino acids. Furthermore, a small amount of vitamins and nucleic acids may be included in medium.

[0041] In the expression system of this invention, high-titer P-450 enzymes with expected activity can be obtained when P-450 enzymes are induced at a temperature of about 25°C or less, preferably at 20 to 24°C, after host *Escherichia coli* has been cultivated at a temperature suitable for the growth of *Escherichia coli*, e.g. at 28 to 40°C.

[0042] The following is a detailed explanation of an example of construction of expression system for *moxA* gene originated from *Microtetraspora recticatena* IFO 14525 which encodes a compactin-hydroxylating enzyme as an instance of actinomycete cytochrome P-450 enzymes. This invention is, however, not restricted at all by this example.

Polymerase Chain Reaction (PCR):

[0043] In the following example, PCT is conducted under conditions as follows.

(1) Condition where genomic DNA is used as a template:

[0044]

(Composition of reaction liquid)	
Sterilized purified water	15 μ l
Twice-concentrated GC buffer I (Takara Shuzo)	25 μ l
dNTP mixed solution (dATP, dGTP, dTTP, dCTP each 2.5 mM)	8 μ l
Forward primer (100 pmol/ μ l)	0.5 μ l
Reverse primer (100 pmol/ μ l)	0.5 μ l
Genomic DNA (10 ng/ μ l)	0.5 μ l
LA Taq (5 units/ μ l Takara Shuzo)	0.5 μ l

(Temperature condition)	
94°C	3 minutes
(98°C 20 seconds; 63°C 30 seconds; 68°C 2 minutes) 30 cycles	
72°C	5 minutes

(2) Condition where plasmid DNA (pMoxAB-fdr1) is used as a template:

[0045]

(Composition of reaction liquid)	
Sterilized purified water	15 μ l
Twice-concentrated GC buffer I (Takara Shuzo)	25 μ l
dNTP mixed solution (dATP, dGTP, dTTP, dCTP each 2.5 mM)	8 μ l
Mox-3F primer (100 pmol/ μ l)	0.5 μ l
Mox-5R primer (100 pmol/ μ l)	0.5 μ l
Plasmid DNA (1 ng/ μ l)	0.5 μ l
LA Taq (5 units/ μ l Takara Shuzo)	0.5 μ l

(Temperature condition)	
94°C	3 minutes
(98°C 20 seconds; 63°C 30 seconds; 68°C 2 minutes) 25 cycles	
72°C	5 minutes

Example 1 Construction of plasmid

(1) pT7-fdr1

[0046] PCR was carried out with use of primer FDR1-1F (5'-GCCATATGACTAGTGCGCCTCACAGACTGGAACG-GGAATCTCATG -3') (see Sequence No. 3) and FDR1-2R (5'-GCGAATTCTGTCTCGGTCAGGCCTGGTCTCCCGTCG-GCCG-3') (see Sequence No. 4) by using, as a template, genomic DNA of *Streptomyces coelicolor* A3(2) [imparted by John Innes Institute (Norwich, UK)], and, thus, there was amplified a 1.3-kb fragment of gene (hereinafter referred

to as *fdr-1*; see Sequence No. 5) encoding a protein which has homology with ferredoxin reductases. This fragment was treated with restriction enzyme *Nde* I and *Bam* HI, and was then subjected to electrophoresis in 0.8 % agarose gel. After the electrophoresis was over, the *fdr-1* gene fragment was recovered, with use of SUPREC-01 (Takara Shuzo), from a gel piece containing said gene fragment, which had been cut out from the gel, and was purified. Said fragment was ligated to *Nde* I site and *Bam* HI site of *Escherichia coli* plasmid vector pET11a (manufactured by Stratagene Co.) with use of T4 DNA ligase, and, then, *Escherichia coli* DH5 α was transformed with the resultant DNA reaction liquid, and, thus, pT7-fdr1 was constructed.

(2) pT7-fdr2

[0047] Under the same condition, PCR was carried out with use of primer FDR2-3F (5'-CGACTAGTGACGAGGAG-GCAGACAAATGGTCGACGCGGATCAG-3') (see Sequence No. 6) and FDR2-4R (5'-CGGGATCCGACAACTAT-GCGACGAGGCTTTGAGGG-3') (see Sequence No. 7) by using genomic DNA of the above-mentioned *Streptomyces coelicolor* A3(2), and, thus, there was amplified a 1.3-kb fragment of gene (hereinafter referred to as *fdr-2*, see Sequence No. 8), which is different from *fdr-1*, encoding a protein which has homology with ferredoxin reductases. This fragment was treated with restriction enzyme *Bam* HI and *Spe* I, and was then subjected to electrophoresis in 0.8 % agarose gel. After the electrophoresis was over, *fdr-1* gene fragment was recovered, with use of SUPREC-01 (Takara Shuzo), from a gel piece containing said gene fragment, which had been cut out from the gel, and was purified. Apart from that, plasmid pT7-fdr1 was treated with *Bam* HI and *Spe* I, and was then subjected to electrophoresis in 0.8 % agarose gel. After the electrophoresis was over, pET11a vector fragment was recovered, with use of SUPREC-01 (Takara Shuzo), from a gel piece containing said vector fragment which had been cut out from the gel, and was purified. Said vector fragment and the above-mentioned *fdr-1* gene fragment were ligated to each other with use of T4 DNA ligase, and, then, *Escherichia coli* DH5 α was transformed, and, thus, pT7-fdr2 was constructed.

(3) pT7-camAB

[0048] PCR was carried out with use of primer PRR-1F (5'-GCCCCCATATGAACGCAAACGACAACGTGGTCATC-3') (see Sequence No. 9) and PRR-2R (5'-GCGGATCCTCAGGCACTACTCAGTTCAGCTTTGGC-3') (see Sequence No. 10) by using, as a template, genomic DNA of *Pseudomonas putida* ATCC17453, and, thus, there was amplified a 1.65 kb fragment (*camAB* fragment; see Sequence No. 16) which contained putidaredoxin reductase gene (*camA*) and putidaredoxin gene (*camB*) which was just downstream of said *camA*. This fragment was treated with restriction enzyme *Nde* I and *Bam* HI, and was then subjected to electrophoresis in 0.8 % agarose gel. After the electrophoresis was over, *camAB* fragment was recovered, with use of SUPREC-01 (Takara Shuzo), from a gel piece containing said fragment, which had been cut out from the gel, and was purified. Said fragment was ligated to *Nde* I site and *Bam* HI site of *Escherichia coli* plasmid vector pET11a (manufactured by Stratagene Co.) with use of T4 DNA ligase, and, then, *Escherichia coli* DH5 α was transformed, and, thus, pT7-camAB was constructed.

(4) pMoxAB

[0049] PCR was carried out with use of primer Mox-1F (5'-GCCGCCCATATGACGAAGAACGTGCGCCGACGAACTG-3') (see Sequence No. 11) and Mox-12R (5'-GCAGATCTAGTGGCTTCAGGCGTCCCGCAGGATGG-3') (see Sequence No. 12) by using, as a template, genomic DNA of IFO14525 strain, and, thus, there was amplified a 1.4-kb fragment (*moxAB* fragment) which contained a gene (*moxA*) encoding compactin-hydroxylation enzyme and ferredoxin gene (*moxB*) which was adjacent downstream thereto. This fragment was treated with restriction enzyme *Nde* I and *Bgl* II, and was then subjected to electrophoresis in 0.8 % agarose gel. After the electrophoresis was over, *moxAB* fragment was recovered, with use of SUPREC-01 (Takara Shuzo), from a gel piece containing said fragment, which had been cut out from the gel, and was purified. Said fragment was ligated to *Nde* I site and *Bam* HI site of the above-mentioned plasmid pET11a with use of T4 DNA ligase, and, then, *Escherichia coli* DH5 α was transformed with resultant reaction liquid, and, thus, plasmid pMoxAB was constructed.

(5) pMoxAB-fdr1 and pMoxAB-fdr2

[0050] PCR was carried out with use of primer Mox-1F (5'-GCCCCCATATGACGAAGAACGTGCGCCGACGAACTG-3') (see Sequence No. 11 as mentioned above) and Mox-2R (5'-CGACTAGTGGCTTCAGGCGTCCCGCAGGATGG-3') (see Sequence No. 13) by using, as a template, genomic DNA of IFO14525 strain, and, thus, there was amplified a 1.4-kb fragment (*moxAB* fragment) which contained a gene (*moxA*) encoding compactin-hydroxylation enzyme and ferredoxin gene (*moxB*) which was adjacent downstream thereto. This fragment was treated with restriction enzyme *Nde* I and *Spe* I, and was then subjected to electrophoresis in 0.8 % agarose gel. After the electrophoresis was over,

moxAB fragment was recovered, with use of SUPREC-01 (Takara Shuzo), from a gel piece containing said fragment, which had been cut out from the gel, and was purified. Said fragment was ligated to *Nde* I site and *Spe* I site of the above-mentioned plasmid pT7-fdr1 with use of T4 DNA ligase, and, then, *Escherichia coli* DH5 α was transformed with resultant reaction liquid, and, thus, plasmid pMoxAB-fdr1 was constructed. Fig. 2 shows the structure of this pMoxAB-fdr1.

[0051] The same inserted fragment was ligated to *Nde* I site and *Spe* I site of another plasmid pT7-fdr2 with use of T4 DNA ligase, and, then, *Escherichia coli* DH5 α was transformed with resultant reaction liquid, and, thus, plasmid pMoxAB-fdr2 was constructed. Fig. 3 shows the structure of this pMoxAB-fdr2.

(6) pMoxAB-camAB

[0052] PCR was carried out with use of primer Mox-3F (5'-GGAGATATACATATGACGAAGAAC-3') (see Sequence No. 14) and Mox-5R (5'-GCCCCCATATGACGCACTCCTAGTGGCTTCAGGCGTCCCG-3') (see Sequence No. 15) by using, as a template, DNA of pMoxAB-fdr1, and, thus, there was amplified a 1.5-kb fragment which contained a gene encoding cytochrome P-450 enzyme having compactin-hydroxylating activity and ferredoxin gene (*moxAB*) which was adjacent downstream thereto. This fragment was ligated to *Nde* I site of the plasmid pT7-camAB with use of T4 DNA ligase, and, then, *Escherichia coli* DH5 α was transformed with resultant reaction liquid, and, thus, plasmid pMoxAB-camAB was constructed. Fig. 4 shows the structure of this pMoxAB-camAB.

Example 2 Preparation of recombinant which has actinomycete cytochrome P-450 enzymatic activity

[0053] *Escherichia coli* BL21(DE3) was transformed with three plasmids, i.e., pMoxAB-fdr1, pMoxAB-fdr2 and pMoxAB-camAB, and, thus, transformant strains corresponding to these plasmids were obtained. Single colony of each of these strains was seeded on 2 ml of LB medium, and was subjected to shake culture at 28°C for 16 hours at 220 rpm. Thus obtained culture liquid in an amount of 200 μ l was mixed with an equal amount (200 μ l) of 40 % glycerol (sterilized) to give a glycerol culture, which was preserved at -80°C until used. On the other hand, with use of pMoxAB and pET11a which was used as a vector, *Escherichia coli* BL21(DE3) was transformed, and, thus, transformant strains corresponding to these plasmids were obtained. Said transformant strains were used as control.

Example 3 Production of pravastatin and its hydroxylated analogues from compactin

(1) Production process with use of static cells:

[0054] Glycerol culture of transformant strain of BL21(DE3) as obtained in the above Example 2 in an amount of 10 μ l was added to 2 ml of LB medium to which 50 μ g/ml (final concentration) of ampicillin had been added, and was then subjected to shake culture at 28°C for 16 hours at 220 rpm. The resultant culture liquid in an amount of 250 μ l was added to 25 ml of NZCYM medium to which 50 μ g/ml (final concentration) of ampicillin had been added, and was then subjected to shake culture at 37°C for 2.5 hours. Then, 25 μ l of 100 mM IPTG and 25 μ l of 80 mg/ml 5-aminolevulinic acid were added in this order, and the resultant mixture was subjected to shake culture at 18-28°C (this temperature is hereinafter called as "induction temperature") for 16 hours at 120 rpm. Cells were recovered by centrifugation from 10 ml of the resultant culture liquid, and were then washed once with conversion buffer-2 (50 mM NaH₂PO₄, 1 mM EDTA, 0.2 mM DTT, 10 % glycerol, [pH 7.3]). Subsequently, the cells were suspended in 1 ml of said buffer to give a suspension of static cells. To this suspension of static cells, there were added compactin sodium salt (final concentration 250 μ g/ml) and NADPH (final concentration 1 mM), and the resultant mixture was incubated at 32°C for 24-48 hours (this time is hereinafter referred to as "conversion time") under shaking condition (220 rpm). Later, to 100 μ l of thus obtained reaction liquid, there was added 100 μ l of acetonitrile, and the resultant mixture was subjected to vortex for one minute at room temperature, and was then centrifuged for 10 minutes at 16,000 rpm with an Ependorf centrifugator. So obtained supernatant was analyzed with HPLC, and, thus, there were detected pravastatin and other hydroxylated analogues which had been formed by the hydroxylation of substrate compactin. The following shows detailed condition for this HPLC.

Analytical apparatus	Shimadzu C-4RA Chromatopac
Column	J' sphere ODS-H80 (YMC, Inc.), 75 mm x 4.6 mm I.D.
Mobile phase A	Ion-exchange water/acetic acid/triethylamine = 998:1:1
B	Methanol/acetic acid/triethylamine = 998:1:1

Gradient time program	0 minute Mobile phase A/B = 50:50
	3.00 minute Mobile phase A/B = 10:90
	3.50 minute Mobile phase A/B = 10:90
	3.51 minute Mobile phase A/B = 50:50
	6.00 minute End

Flow rate	2.0 ml/minute
Detection	UV 237 nm
Injection content	10 µl
Column temperature	40°C
Analysis time	6 minutes
Retention time	compactin 4.2 minutes
	pravastatin 2.7 minutes
	RT-5.8 substances 3.6 minutes

(2) Production process by Fed-batch method:

[0055] Glycerol culture of transformant strain of BL21(DE3) in an amount of 10 µl was added to 2 ml of LB medium to which 50 µg/ml (final concentration) of ampicillin had been added, and was then subjected to shake culture at 28°C for 16 hours at 220 rpm. The resultant culture liquid in an amount of 250 µl was added to 25 ml of M9-plus medium (M9 salt, 0.4 % glucose, 0.5 % casamino acids, 100 µg/ml thiamin, 20 µl/ml thymine, 0.1 mM CaCl₂, 1 mM MgCl₂) to which 50 µg/ml (final concentration) of ampicillin had been added, and was then subjected to shake culture at 37°C for 2.5 hours. Then, 25 µl of 100 mM IPTG and 25 µl of 80 mg/ml 5-aminolevulinic acid were added in this order, and the resultant mixture was subjected to shake culture at 22°C for 16 hours at 120 rpm. To the resultant culture liquid, there was added 2.5 ml of conversion mixture (2.5 mg/ml compactin sodium salt, 1 mg/ml FeSO₄·7H₂O, 10 mM NADPH, 50 % glycerol), and, thus, cultivation was continued at 22°C for 96 hours. The period of time which has passed after the addition of this conversion mixture is hereinafter referred to as "cultivation time". Then, to 100 µl of this culture liquid, there was added 100 µl of acetonitrile, and the resultant mixture was subjected to vortex for one minute at room temperature, and was then centrifuged for 10 minutes at 16,000 rpm with an Epfendorf centrifugator. So obtained supernatant was analyzed with HPLC, and, thus, there were detected pravastatin and other hydroxylated analogues which had been formed by the hydroxylation of substrate compactin.

[0056] Table 1 shows results of the measurement of the amount of pravastatin and RT-5.8 substance produced by static cells as mentioned in Example 3(1) with use of *Escherichia coli* transformant strain, under the protein induction condition of 18-28°C and with a conversion time of 48 hours.

Table 1

Induction temperature	18°C		22°C		25°C		28°C	
	Pravastatin	RT-5.8 substances	Pravastatin	RT-5.8 substances	Pravastatin	RT5.8 substances	Pravastatin	RT-5.8 substances
Hydroxylated compactin (µg/ml)								
BL21(DE3)/ pET11a	0	0	0	0	0	0	0	0
BL21(DE3)/ pMoxAB	0	0.18	0	0	0	0	0	0.3
BL21(DE3)/ pMoxAB-fdr1	0.24	1.24	1.72	8.48	0.43	1.92	0	0.61
BL21(DE3)/ pMoxAB-fdr2	0.25	1.31	2.15	10.21	0	0.84	0.35	1.65
BL21(DE3)/ pMoxAB-camAB	3.84	22.07	6.09	33.55	4.05	16.53	0.97	5.49

[0057] Productivity was the highest when induction temperature was 22°C, under which condition each of strains wherein *Streptomyces coelicolor* A3(2)-originated ferredoxin reductase (*fdr-1* or *fdr-2*) had been co-expressed accumulated, in medium, 1.7 to 2.1 µg/ml of pravastatin and 8.4 to 10.2 µg/ml of RT-5.8 substances. A strain wherein *camAB* had been expressed showed much higher productivity; it accumulated, in medium, 6.09 µg/ml of pravastatin and 33.55 µg/ml of RT-5.8 substance. In the case where there was used, as control, vector alone (BL21(DE3)/pET11a) or a strain which contained no gene to encode ferredoxin reductase (BL21(DE3)/pMoxAB), there were hardly detected pravastatin and RT-5.8 substances.

[0058] Table 2 shows results of test of productivity of pravastatin in Fed-batch method as mentioned in Example 4 (2).

Table 2

Cultivation time	4 hours		24 hours		48 hours		96 hours	
	Pravastatin	RT-5.8 substances	Pravastatin	RT-5.8 substances	Pravastatin	RT-5.8 substances	Pravastatin	RT-5.8 substances
Hydroxylated compactin ($\mu\text{g/ml}$)								
BL21(DE3)/pET11a	0	0	0	0	0	0	0	0
BL21(DE3)/pMoxAB	0	0	0	0	0	0	0	0
BL21(DE3)/pMoxAB-fdr1	0	0	0	0	0	0.87	0	0.61
BL21(DE3)/pMoxAB-fdr2	0	0	0	0	0	0.29	0	0.28
BL21(DE3)/pMoxAB-camAB	0	0	0.28	2.82	0.64	7.74	0.95	12.44

[0059] In the results with cultivation time of 96 hours, strains wherein *Streptomyces coelicolor* A3(2)-originated ferredoxin reductase (*fdr-1* or *fdr-2*) had been co-expressed accumulated, in medium, 0.28 to 0.61 µg/ml of RT-5.8 substances while accumulating no pravastatin. A strain wherein *camAB* had been expressed showed high productivity; it accumulated, in medium, 0.95 µg/ml of pravastatin and 12.44 µg/ml of RT-5.8 substances. In the case where there was used, as control, vector alone (BL21(DE3)/pET11a) or a strain which contained no gene to encode ferredoxin reductase (BL21(DE3)/pMoxAB), pravastatin and RT-5.8 substances were not detected.

[0060] In a strain wherein *camAB* had been co-expressed, i.e., in *Escherichia coli* wherein pMoxAB-*camAB* had been introduced, *moxB* (ferredoxin gene) and *camB* (putidaredoxin gene) among thus introduced genes overlap with each other in their function. In order to know which gene among the constituent genes contained in said pMoxAB-*camAB* are indispensable for the expression of activity, the inventors of this invention constructed a plasmid which lacked one or two of said constituent genes, and introduced the plasmid into *Escherichia coli*. Table 3 shows results of productivity of hydroxylated compactin with use of static cells of thus prepared strain, and with a conversion time of 24 hours.

Table 3

	Constituent gene (+: existent; -: non-existent)				Hydroxylated compactin (µg/ml)	
	<i>moxA</i>	<i>moxB</i>	<i>camA</i>	<i>camB</i>	Pravastatin	RT-5.8 substances
BL21(DE3)/ pET11a	-	-	-	-	0	0
BL21(DE3)/ pMoxAB	+	+	-	-	0	0
BL21(DE3)/ pMoxAB- <i>camA</i>	+	+	+	-	0.17	0.82
BL21(DE3)/ pMoxA- <i>camAB</i>	+	-	+	+	0	0
BL21(DE3)/ pMoxAB- <i>camAB</i>	+	+	+	+	1.67	9.96

[0061] The above shows that three kinds of gene of *moxA*, *moxB* and *camA* are essential for the expression of activity, and that the addition of *camB* achieves a remarkable increase in activity; the yield of hydroxylated compactin increased about 10 times.

Example 5 Construction of plasmid

(1) pT7NS-*camAB*

[0062] PCR was carried out under the following condition with use of primer PRR-1F (5'-GCCCCCATATGAACG-CAAACGACAACGTGGTCATC-3') (see Sequence No. 9) and PRR-2R (5'-GCGGATCCTCAGGCACTACTCAGT-TCAGCTTTGGC-3') (see Sequence No. 10) by using, as a template, genomic DNA of *Pseudomonas putida* ATCC17453.

(Composition of reaction liquid)	
Sterilized purified water	15 µl
Twice-concentrated GC buffer I (Takara Shuzo)	25 µl
dNTP mixed solution (dATP, dGTP, dTTP, dCTP each 2.5 mM)	8 µl
PRR-1F primer (100 pmol/µl)	0.5 µl
PRR-2R primer (100 pmol/µl)	0.5 µl
<i>Pseudomonas putida</i> ATCC 17453 Genomic DNA (10 ng/µl)	0.5 µl
LA Taq (5 units/µl Takara Shuzo)	0.5 µl

(Temperature condition)	
95°C	3 minutes
(98°C 20 seconds; 63°C 30 seconds; 68°C 2 minutes) 30 cycles	
72°C	5 minutes

[0063] An amplified 1.5-kb fragment (*camAB* fragment) which contained ferredoxin reductase gene (*camA*) and putidaredoxin gene (*camB*) just downstream thereto was treated with restriction enzyme *Nde* I and *Bam* HI, and was then subjected to electrophoresis in 0.8 % agarose gel. After the electrophoresis was over, *camAB* fragment was recovered, with use of SUPREC-01 (Takara Shuzo), from a gel piece containing said gene fragment which had been cut out from the gel, and was purified. Said fragment was ligated to *Nde* I site and *Bam* HI site of *Escherichia coli* plasmid vector pET11a (manufactured by Stratagene Co.) with use of T4 DNA ligase, and, then, *Escherichia coli* DH5 α was transformed, and, thus, pT7-*camAB* was constructed. To *Nde* I site of said plasmid pT7-*camAB*, there was ligated by T4 DNA ligase one molecule of linker which had been prepared by the annealing of two kinds of synthetic oligo DNAs SP-1 (5'-TATGCGTCACTAGTCGGGAGTGCGTTA-3') (see Sequence No. 17) and SP-2 (5'-TATAACGCACTCCGACTAGTGACGCA-3') (see Sequence No. 18), with which *Escherichia coli* DH5 α was transformed, and, thus, plasmid pT7NS-*camAB* was constructed. Fig. 5 shows the structure of pT7NS-*camAB*.

(2) pCBM-*camAB*

[0064] PCR was carried out under the following condition with use of primer CB-4F (5'-GCCCCCATATGACAGCTTGAATCTGATG-3') (see Sequence No. 19) and CB-5R (5'-GCACTAGTCAGAGACGGACCGGCAGAC-3') (see Sequence No. 20) by using, as a template, total DNA of *Streptomyces thermotolerans* ATCC11416, and, thus, there was prepared 1.25 kb fragment of ORF-A (cytochrome P-450 gene which encodes enzyme to epoxidize 12- and 13-positions of carbomycin B) (gene sequence of ORF-A and the function of ORF-A are mentioned in Bioscience Biotechnology Biochemistry vol. 59, 582-588, 1995; the contents of this literature is incorporated into the present specification by this citation).

(Composition of reaction liquid)	
Sterilized purified water	61 μ l
10 times-concentrated buffer (Takara Shuzo)	10 μ l
25 mM MgCl_2	10 μ l
dNTP mixed solution (dATP, dGTP, dTTP, dCTP each 2.5 mM)	16 μ l
CB-4F primer (100 pmol/ μ l)	0.5 μ l
CB-5R primer (100 pmol/ μ l)	0.5 μ l
Total DNA (100 ng/ μ l) of <i>Streptomyces thermotolerans</i> ATCC11416	1 μ l
LA Taq (5 units/ μ l, Takara Shuzo)	1 μ l

(Temperature condition)	
95°C	3 minutes
(98°C 20 seconds; 63°C 30 seconds; 68°C 2 minutes) 30 cycles	
72°C	5 minutes

[0065] This gene fragment was digested with restriction enzyme *Nde* I and *Spe* I, and was then subjected to electrophoresis in 0.8 % agarose gel. After the electrophoresis was over, ORF-A fragment was recovered, with use of SUPREC-01 (Takara Shuzo), from a gel piece containing said gene fragment, which had been cut out from the gel, and was purified. Said fragment was ligated to *Nde* I-*Spe* I site of pT7NS-*camAB* with use of T4 DNA ligase, and, with the resultant reaction liquid, *Escherichia coli* DH5 α was transformed, and, thus, plasmid pCBM-*camAB* was constructed. Fig. 6 shows the structure of pCBM-*camAB*.

(3) pSC154A1-*camAB*

[0066] Total DNA of *Streptomyces coelicolor* A3(2) (imparted by John Innes Institute, Norwich, UK) was digested with restriction enzyme *Bam* HI and *Pst* I to give a 100 ng/ μ l solution of TE (10 mM Tris-HCl [pH 8.0], 1 mM EDTA). PCR was carried out under the following condition by using this DNA as a template with use of primer 154A1-1F (5'-GCCCCCATATGGCGACCCAGCAGCCCGCCCTC-3') (see Sequence No. 21) and 154A1-2R (5'-GCACTAGTCAGCCGGCGTGCAGCAGGACCGG-3') (see Sequence No. 22), and, thus, there was prepared 1.2 kb gene fragment which encoded CYP154A1 (DNA sequence of gene which encodes *Streptomyces coelicolor* A3(2)-originated CYP154A1 has been published in gene database, e.g., Gen Bank, under gene name of SCE6.21).

(Composition of reaction liquid)	
Sterilized purified water	61 μ l
10 times-concentrated buffer (Takara Shuzo)	10 μ l
25 mMgCl ₂	10 μ l
dNTP mixed solution (dATP, dGTP, dTTP, dCTP each 2.5 mM)	16 μ l
154A1-1F primer (100 pmol/ μ l)	0.5 μ l
154A1-2R primer (100 pmol/ μ l)	0.5 μ l
Total DNA (100 ng/ μ l) of <i>Streptomyces coelicolor</i> A3(2) digested with <i>Bam</i> HI- <i>Pst</i> I	1 μ l
LA Taq (5 units/ μ l, Takara Shuzo)	1 μ l

(Temperature condition)	
95°C	3 minutes
(98°C 20 seconds; 63°C 30 seconds; 68°C 2 minutes) 30 cycles	
72°C	5 minutes

[0067] This gene fragment was digested with restriction enzyme *Nde* I and *Spe* I, and was then subjected to electrophoresis in 0.8 % agarose gel. After the electrophoresis was over, CYP154A1-encoding gene fragment was recovered, with use of SUPREC-01 (Takara Shuzo), from a gel piece containing said gene fragment which had been cut out from the gel, and was purified. Said fragment was ligated to *Nde* I-*Spe* I site of pT7NS-camAB with use of T4 DNA ligase, and, with the resultant reaction liquid, *Escherichia coli* DH5 α was transformed, and, thus, plasmid pSC154A1-camAB was constructed. Fig. 7 shows the structure of pSC154A1-camAB.

(4) pDoxA1-camAB

[0068] PCR was carried out under the following condition with use of primer DoxA-1F (5'-GCCCCCATATGGCCGTC-GACCCGTTTCGCGTG-3') (see Sequence No. 23) and DoxA-2R (5'-GCACTAGTCAGCGCAGCCAGACGGGCAGTTC-3') (see Sequence No. 24) by using, as a template, total DNA of daunomycin-producing bacterium *Streptomyces peucetius* ATCC 29050, and, thus, there was prepared 1.2-kb fragment of *doxA* (cytochrome P-450 gene which participates in the biosynthesis of daunomycin). DNA sequence of the *doxA* gene is mentioned in Journal of Bacteriology, vol. 181, No. 1, 305-318, 1999 (the contents of this literature is incorporated into the present specification by this citation).

(Composition of reaction mixture)	
Sterilized purified water	61 μ l
10 times-concentrated buffer (Takara Shuzo)	10 μ l
25 mMgCl ₂	10 μ l
dNTP mixed solution (dATP, dGTP, dTTP, dCTP each 2.5 mM)	16 μ l
DoxA-1F primer (100 pmol/ μ l)	0.5 μ l
DoxA-2R primer (100 pmol/ μ l)	0.5 μ l
Total DNA (100 ng/ μ l) of <i>Streptomyces peuceticus</i> ATCC 29050	1 μ l
LA Taq (5 units/ μ l, Takara Shuzo)	1 μ l

(Temperature condition)	
95°C	3 minutes
(98°C 20 seconds; 63°C 30 seconds; 68°C 2 minutes) 30 cycles	
72°C	5 minutes

[0069] This gene fragment was digested with restriction enzyme *Nde* I and *Spe* I, and was then subjected to electrophoresis in 0.8 % agarose gel. After the electrophoresis was over, *doxA* fragment was recovered, with use of SU-PREC-01 (Takara Shuzo), from a gel piece containing said gene fragment which had been cut out from the gel, and was purified. Said fragment was ligated to *Nde* I-*Spe* I site of pT7NS-camAB with use of T4 DNA ligase, and, with the resultant reaction liquid, *Escherichia coli* DH5 α was transformed, and, thus, plasmid pDoxA1-camAB was constructed. Fig. 8 shows the structure of pDoxA1-camAB.

Example 6 Microbial conversion with use of *Escherichia coli* recombinant wherein cytochrome P-450 had been expressed

(1) Production of carbomycin A

[0070] Glycerol culture, in an amount of 10 μ l, of *Escherichia coli* BL21(DE3) strain which had been transformed with pCBM-camAB among the plasmids as obtained in the above-mentioned Example 4 was added to 2 ml of LB medium to which 50 μ g/ml (final concentration) of ampicillin had been added, and the resultant mixture was subjected to shake culture at 28°C for 16 hours at 220 rpm. Thus obtained culture liquid in an amount of 250 μ l was added to 25 ml of NZCYM medium to which 50 μ g/ml of ampicillin had been added, and the resultant mixture was subjected to shake culture at 37°C for 2.5 hours. Then, 25 μ l of 100 mM IPTG and 25 μ l of 80 mg/ml δ -aminolevulinic acid were added in order, and the resultant mixture was subjected to shake culture at 22°C at 120 rpm for 16 hours. Cells were recovered by centrifugation from the resultant culture liquid, and were then washed once with conversion buffer-2 (50 mM NaH₂PO₄, 1 mM EDTA, 0.2 mM DTT, 10 % glycerol, [pH 7.3]). Subsequently, the cells were suspended in 3 ml of said buffer to give a suspension of static cells. To 600 μ l of this suspension of static cells, 3 μ l of 100 mg/ml methanol solution of carbomycin B was added, and the resultant mixture was incubated at 28°C for five hours with shaking (220 rpm). Later, to thus obtained reaction liquid, there was added 100 μ l of 50 % K₂HPO₄ (pH 8.5) and 100 μ l of ethyl acetate, and the resultant mixture was subjected to vortex, and then to centrifugation for five minutes at 16,000 rpm with an Eppendorf centrifugator. A TLC plate was spotted with 10 μ l of so obtained ethyl acetate phase, and was then subjected to development with a developer (ethyl acetate : diethylamine = 100:2). Subsequently, this plate was sprayed with 10 % sulfuric acid, and heated at 100°C for 10 minutes. Spots on which color had come out were analyzed for coloring intensity with a dual-wavelength chromatoscanner CS-930 (manufactured by Shimadzu Seisakusho) at a wavelength of 600 nm, and, thus, there was evaluated the amount of carbomycin A (RF value in TLC: 0.64) which had been formed by the epoxidation of substrate carbomycin B (RF value in TLC: 0.71). As a result, it was confirmed that carbomycin A had been formed with a yield of 90 μ g/ml. Then, substrate conversion reaction was conducted with use of a control strain BL21(DE3) (pET11a) under the same condition as stated above. As a result of analysis, no formation of carbomycin A was detected.

(2) De-ethylation of 7-ethoxycoumarin

[0071] Glycerol culture, in an amount of 10 μ l, of *Escherichia coli* BL21(DE3) strain which had been transformed with pSC154A1-camAB among the plasmids as obtained in the above-mentioned Example 5 was added to 2 ml of LB medium to which 50 μ g/ml (final concentration) of ampicillin had been added, and the resultant mixture was subjected to shake culture at 28°C for 16 hours at 220 rpm. Thus obtained culture liquid in an amount of 250 μ l was added to 25 ml of NZCYM medium to which 50 μ g/ml of ampicillin had been added, and the resultant mixture was subjected to shake culture at 37°C for 2.5 hours. Then, 25 μ l of 100 mM IPTG and 25 μ l of 80 mg/ml δ -aminolevulinic acid were added in order, and the resultant mixture was subjected to shake culture at 22°C at 120 rpm for 16 hours. Cells were recovered by centrifugation from the resultant culture liquid, and were then washed once with conversion buffer-2 (50 mM NaH₂PO₄, 1 mM EDTA, 0.2 mM DTT, 10 % glycerol, [pH 7.3]). Subsequently, the cells were suspended in 6 ml of said buffer to give a suspension of static cells. To 1 ml of this suspension of static cells, 5 μ l of 50 mM DMSO solution of 7-ethoxycoumarin was added, and the resultant mixture was incubated at 28°C for five hours with shaking (220 rpm). Later, to thus obtained reaction liquid, there was added 200 μ l of ethyl acetate, and the resultant mixture was subjected to vortex, and then to centrifugation for five minutes at 16,000 rpm with an Eppendorf centrifugator. There was taken out 100 μ l of so obtained ethyl acetate phase, which was then evaporated to dryness in vacuum. The resultant dried pellet was dissolved in 1 ml of 100 mM potassium phosphate buffer (pH 7.4). Thus obtained solution was 80-times diluted, and was then measured for fluorescence (wavelength: 460 nm) with F-2000 spectrophotofluorometer (manufactured by Hitachi Science Systems, Co.) at an excitation wave length of 380 nm for the purpose of evaluation of the amount of 7-hydroxycoumarin which had been formed by de-ethylation of substrate 7-ethoxycoumarin. As a result, fluorescence intensity was 2770, and, thus, the formation of 7-hydroxycoumarin was confirmed. Then, substrate conversion reaction was conducted with use of a control strain BL21(DE3) (pET11a) under the same condition as stated above. As a result of analysis, fluorescence intensity was three or less.

(3) Dehydrogenation of 13-dihydrodaunomycin

[0072] Glycerol culture, in an amount of 10 μ l, of *Escherichia coli* BL21(DE3) strain which had been transformed by pDoxA1-camAB among the plasmids as obtained in the above-mentioned Example 5 was added to 2 ml of LB medium to which 50 μ g/ml (final concentration) of ampicillin had been added, and the resultant mixture was subjected to shake culture at 28°C for 16 hours at 220 rpm. Thus obtained culture liquid in an amount of 250 μ l was added to 25 ml of NZCYM medium to which 50 μ g/ml of ampicillin had been added, and the resultant mixture was subjected to shake culture at 37°C for 2.5 hours. Then, 25 μ l of 100 mM IPTG and 25 μ l of 80 mg/ml δ -aminolevulinic acid were added in order, and the resultant mixture was subjected to shake culture at 22°C at 120 rpm for 24 hours. Cells were recovered by centrifugation from the resultant culture liquid, and were then washed once with conversion buffer-2 (50 mM NaH_2PO_4 , 1 mM EDTA, 0.2 mM DTT, 10 % glycerol, [pH 7.3]). Subsequently, the cells were suspended in 4 ml of said buffer to give a suspension of static cells. To 1 ml of this suspension of static cells, 10 μ l of 10 mg/ml methanol solution of 13-dihydrodaunomycin was added, and the resultant mixture was incubated at 28°C for 24 hours with shaking (220 rpm). Later, to 400 μ l of thus obtained reaction liquid, there was added 1.2 ml of acetone, and the resultant mixture was subjected to vortex, and was then extracted with 300 μ l of chloroform. Thus obtained extract was evaporated to dryness in vacuum, and was then dissolved in 500 μ l of 0.3 M hydrochloric acid, and thus obtained solution was heated at 80°C for 30 minutes. This solution was extracted with 100 μ l of chloroform, and thus obtained extract was evaporated to dryness in vacuum. The resultant dried pellet was dissolved in 100 μ l of methanol, and the resultant solution was subjected to HPLC under the following condition, and, thus, there was detected daunomycin which had been formed by the dehydrogenation of substrate 13-dihydrodaunomycin.

(Analytical condition of HPLC)

[0073]

Analytical apparatus	Shimadzu LC10 Chromatopac (manufactured by Shimadzu Seisakusho)	
Column	ZORBAX TMS (5 μ) 4.6 mm \times 250 mm I.D.	
Mobile phase	To a mixture of water/acetonitrile/methanol/phosphoric acid = 540:290:170:2 (volume ratio), 1.0 g of sodium lauryl sulfate was added and dissolved, and, to the resultant mixture, 2N NaOH was added for the adjustment of pH to 3.6.	
Flow rate	1.5 ml/minute	
Wavelength for detection	254 nm	
Injection content	20 μ l	
Column temperature	40°C	
Analysis time	20 minutes	
Retention time	13-dihydrodaunomycin	4.8 minutes
	daunomycin	5.9 minutes

[0074] Analysis detected 3.7 μ g/ml of daunomycin. Then, substrate conversion reaction was conducted with use of a control strain BL21(DE3) (pET11a) under the same condition as stated above. As a result of analysis, no formation of daunomycin was detected.

Industrial applicability

[0075] In accordance with this invention, single oxygen atom insertional reaction of organic compound as a substrate can efficiently be conducted with use of a recombinant which has been constructed by use of actinomycete cytochrome P-450 gene and *Escherichia coli* as a host.

[0076] This invention also provides a gene library suitable as an objective of high throughput screening or other simple and rapid enzymatic assay screening for the screening of industrially important and desired actinomycete P-450 enzymes.

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<120> EXPRESSION SYSTEM OF ACTINOMYCETE-ORIGIN CYTOCHROME
P-450 IN ESCHERICHIA COLI

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Pro His Gln Cys Leu Gly Gln Asn Leu Ala Arg Met Glu Leu Gln Ile
355 360 365
Val Phe Asp Thr Leu Phe Arg Arg Ile Pro Ser Leu Arg Leu Ala Val
370 375 380
55 Pro Met Glu Asp Val Pro Phe Lys Gly Asp Ser Val Ile Tyr Gly Val
385 390 395 400

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His Glu Leu Pro Val Thr Trp
405

5 <210> 3
<211> 65
<212> PRT
<213> Microtetraspora recticatena IFO14525

10 <400> 3
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1 5 10 15
Val Leu Thr Glu Pro Ala Val Phe Asp Gln Asp Asp Asp Gly Ile Val
20 25 30
Ala Leu Leu Thr Asp His Pro Asp Asp Gln Ser Ala Ala Gln Val Arg
15 35 40 45
His Ala Val Thr Leu Cys Pro Ser Arg Ala Leu Ser Ile Leu Arg Asp
50 55 60
Ala
65

20 <210> 4
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<212> DNA
25 <213> Streptomyces sp.TM-7

<220>
<221> CDS
<222> (544)..(1761)

30 <220>
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<222> (1782)..(1970)

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35 tcgccggggcc cggcggtgtg gaccgttcgc ggaccagccg ggccaattcg gggtcgtgca 60
tgacctcggt gagcaggccg cggagtatgt ccgccgtgcg aggcggccaa cctggcgagg 120
agtcgccgta gcgcggtgat gacatcggtg cgcaggcgcc cgggtgtcggg caggtcggcg 180
40 tcggacagcc ggtgggcccgc gcaggcgctc acgacgagtt cggcacggcc gggccacctc 240
cggtagcaggg tggccttgcc ggtacggggc cgtgcggcca cgcgtccat cgtcagtc 300
ggcgtagtcc gacctcggtc agtttcctcg agggtcgcgg ccaggatggc cctctccagt 360
45 tcctctctc ggccggcgag ggtttttcga tggtcgcggt cgtccgggtcc ggcgcgtccc 420
cgtggggttg aggcattgact ccagccatt tgcgagcac ccgttgtgag cgtcgggtgg 480
gtaagcctag ccttcggtta gagaactgac cgttctttaa gcgtcgagt catcgaggga 540
50 ccg atg acc gag acc gtt acg acg ccc aca tca ggc gcc ccc gcc ttc 588
Met Thr Glu Thr Val Thr Thr Pro Thr Ser Gly Ala Pro Ala Phe
1 5 10 15
ccc agt gac cgc acc tgc ccc tac cac ctc ccc gac cgg tac aac gac 636
55 Pro Ser Asp Arg Thr Cys Pro Tyr His Leu Pro Asp Arg Tyr Asn Asp
20 25 30

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	ctc cgg gac cgg gag ggt tgc ctg cag cgg gtc acc ctc tac gac ggc	684
	Leu Arg Asp Arg Glu Gly Ser Leu Gln Arg Val Thr Leu Tyr Asp Gly	
	35 40 45	
5	cgg cag gca tgg ctg gtg acc ggg tac gac acg gca cgc aag ctg ctg	732
	Arg Gln Ala Trp Leu Val Thr Gly Tyr Asp Thr Ala Arg Lys Leu Leu	
	50 55 60	
10	gcc gac ccc cgg ctc tgc tcc gac cgg aca cac gcc gac ttc ccc gcc	780
	Ala Asp Pro Arg Leu Ser Ser Asp Arg Thr His Ala Asp Phe Pro Ala	
	65 70 75	
	acc tcc ggg cgg gtg gag agc ttc cgg gac cgc cgg ccg gcg ttc atc	828
	Thr Ser Gly Arg Val Glu Ser Phe Arg Asp Arg Arg Pro Ala Phe Ile	
15	80 85 90 95	
	agc ctg gac ccg ccc gag cac ggg ccg aaa cgg cgc cat gac cat cag	876
	Ser Leu Asp Pro Glu His Gly Pro Lys Arg Arg His Asp His Gln	
	100 105 110	
20	gag ttc acc gtc cgg cgc atc aag ggc atg cgg gcc gac gtc gag cag	924
	Glu Phe Thr Val Arg Arg Ile Lys Gly Met Arg Ala Asp Val Glu Gln	
	115 120 125	
	atc gtg cac ggc ttc ctg gac gag atg atc gca ggc ggc ccg ccc gcc	972
	Ile Val His Gly Phe Leu Asp Glu Met Ile Ala Gly Gly Pro Pro Ala	
25	130 135 140	
	gac ctg gtc agc cag ttc gcg ctg ccg gtc ccg tcc ctg gtg atc tgc	1020
	Asp Leu Val Ser Gln Phe Ala Leu Pro Val Pro Ser Leu Val Ile Cys	
	145 150 155	
30	cgt ctg ctc ggt gtg ccc tac gcg gac cac gac ttc ttc cag gac gcc	1068
	Arg Leu Leu Gly Val Pro Tyr Ala Asp His Asp Phe Phe Gln Asp Ala	
	160 165 170 175	
	agc gca cgg ctg atc cag tcc ccg gac gcg gcg ggt gcg cgt gcc gcc	1116
	Ser Ala Arg Leu Ile Gln Ser Pro Asp Ala Ala Gly Ala Arg Ala Ala	
35	180 185 190	
	cgg gac gac ctg gag agc tat ctg ggc gct ctg gtg gac agc ctg cga	1164
	Arg Asp Asp Leu Glu Ser Tyr Leu Gly Ala Leu Val Asp Ser Leu Arg	
	195 200 205	
40	ggc gag tcc cgg ccg ggc ctg ctg agc acg ctc gtc agg gag cag ctg	1212
	Gly Glu Ser Arg Pro Gly Leu Leu Ser Thr Leu Val Arg Glu Gln Leu	
	210 215 220	
	gag aag ggc gcg atc gac cgg gag gag ctg gtg tgc acg gcg atc ctg	1260
	Glu Lys Gly Ala Ile Asp Arg Glu Glu Leu Val Ser Thr Ala Ile Leu	
45	225 230 235	
	ctg ctg gtc gcc gga cac gag gcg acg gcg tgc atg acg tgc ctc agc	1308
	Leu Leu Val Ala Gly His Glu Ala Thr Ala Ser Met Thr Ser Leu Ser	
50	240 245 250 255	
	gtc atc acc ctc ctc gaa cat ccc gac cag cac gcc gcg ttg cgc gcc	1356
	Val Ile Thr Leu Leu Glu His Pro Asp Gln His Ala Ala Leu Arg Ala	
	260 265 270	
55	gat ccg tgc ctg gtg ccc ggc gcg gtg gag gag ctg ctg cgc tat ctg	1404
	Asp Pro Ser Leu Val Pro Gly Ala Val Glu Glu Leu Leu Arg Tyr Leu	
	275 280 285	

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5 gcc atc gcc gac atc gcc ggc ggg cgg atc gcg acg gcg gac atc gag 1452
Ala Ile Ala Asp Ile Ala Gly Gly Arg Ile Ala Thr Ala Asp Ile Glu
290 295 300

atc gac ggg cag cgc atc cgg gcg ggg gag ggg gtc atc gtc acc aac 1500
Ile Asp Gly Gln Arg Ile Arg Ala Gly Glu Gly Val Ile Val Thr Asn
305 310 315

10 tcg atc gcc aac cgc gac ggc tcc gtc ttc gcc gac ccg gac gcc ttc 1548
Ser Ile Ala Asn Arg Asp Gly Ser Val Phe Ala Asp Pro Asp Ala Phe
320 325 330 335

15 gac gtg cgg cgc gag gcc cgc cac cac ctg gcg ttc ggc tac ggg gtg 1596
Asp Val Arg Arg Glu Ala Arg His His Leu Ala Phe Gly Tyr Gly Val
340 345 350

cat cag tgc ctc ggc cag aac ctg gcc cgc ctc gaa ctg gag gtc atc 1644
His Gln Cys Leu Gly Gln Asn Leu Ala Arg Leu Glu Leu Glu Val Ile
355 360 365

20 ctc acg gcg ctg ttc gag cgg ctg ccc ggt ctg cgg ctg gcg gtg ccg 1692
Leu Thr Ala Leu Phe Glu Arg Leu Pro Gly Leu Arg Leu Ala Val Pro
370 375 380

25 gtg gac cgg ctg acc ctg cgc ccg ggc acg acg atc cag ggc gtg aac 1740
Val Asp Arg Leu Thr Leu Arg Pro Gly Thr Thr Ile Gln Gly Val Asn
385 390 395

30 gaa ctc ccg gtc acc tgg tga ccgcggcgaa aggagcagcc atg cgt gtg acg 1793
Glu Leu Pro Val Thr Trp Met Arg Val Thr
400 405 410

gcc gac cgg gag gtc tgc gtg gga gcg ggc ctg tgc gcc ttg acg gcg 1841
Ala Asp Arg Glu Val Cys Val Gly Ala Gly Leu Cys Ala Leu Thr Ala
415 420 425

35 ccg gag gtc ttc gac cag gac gac gac ggt gtg gtg acg gtg ctg gcc 1889
Pro Glu Val Phe Asp Gln Asp Asp Asp Gly Val Val Thr Val Leu Ala
430 435 440

40 gcg gaa ccc ggc gag gcc ggc cgt gcg gcg gca ctc gaa gcc ggc gtg 1937
Ala Glu Pro Gly Glu Ala Gly Arg Ala Ala Ala Leu Glu Ala Gly Val
445 450 455

ctg tgc ccg tcc ggc gcg gta cgc gtc gtc gag tagggggccgt gcggggccgt 1990
Leu Cys Pro Ser Gly Ala Val Arg Val Val Glu
460 465

45 ga 1992

<210> 5
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50 <212> PRT
<213> Streptomyces sp.TM-7

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Met Thr Glu Thr Val Thr Thr Pro Thr Ser Gly Ala Pro Ala Phe Pro
1 5 10 15
55 Ser Asp Arg Thr Cys Pro Tyr His Leu Pro Asp Arg Tyr Asn Asp Leu
20 25 30

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Arg Asp Arg Glu Gly Ser Leu Gln Arg Val Thr Leu Tyr Asp Gly Arg
35 40 45
Gln Ala Trp Leu Val Thr Gly Tyr Asp Thr Ala Arg Lys Leu Leu Ala
50 55 60
5 Asp Pro Arg Leu Ser Ser Asp Arg Thr His Ala Asp Phe Pro Ala Thr
65 70 75 80
Ser Gly Arg Val Glu Ser Phe Arg Asp Arg Arg Pro Ala Phe Ile Ser
85 90 95
10 Leu Asp Pro Pro Glu His Gly Pro Lys Arg Arg His Asp His Gln Glu
100 105 110
Phe Thr Val Arg Arg Ile Lys Gly Met Arg Ala Asp Val Glu Gln Ile
115 120 125
Val His Gly Phe Leu Asp Glu Met Ile Ala Gly Gly Pro Pro Ala Asp
130 135 140
15 Leu Val Ser Gln Phe Ala Leu Pro Val Pro Ser Leu Val Ile Cys Arg
145 150 155 160
Leu Leu Gly Val Pro Tyr Ala Asp His Asp Phe Phe Gln Asp Ala Ser
165 170 175
Ala Arg Leu Ile Gln Ser Pro Asp Ala Ala Gly Ala Arg Ala Ala Arg
180 185 190
20 Asp Asp Leu Glu Ser Tyr Leu Gly Ala Leu Val Asp Ser Leu Arg Gly
195 200 205
Glu Ser Arg Pro Gly Leu Leu Ser Thr Leu Val Arg Glu Gln Leu Glu
210 215 220
Lys Gly Ala Ile Asp Arg Glu Glu Leu Val Ser Thr Ala Ile Leu Leu
225 230 235 240
25 Leu Val Ala Gly His Glu Ala Thr Ala Ser Met Thr Ser Leu Ser Val
245 250 255
Ile Thr Leu Leu Glu His Pro Asp Gln His Ala Ala Leu Arg Ala Asp
260 265 270
Pro Ser Leu Val Pro Gly Ala Val Glu Glu Leu Leu Arg Tyr Leu Ala
275 280 285
30 Ile Ala Asp Ile Ala Gly Gly Arg Ile Ala Thr Ala Asp Ile Glu Ile
290 295 300
Asp Gly Gln Arg Ile Arg Ala Gly Glu Gly Val Ile Val Thr Asn Ser
305 310 315 320
Ile Ala Asn Arg Asp Gly Ser Val Phe Ala Asp Pro Asp Ala Phe Asp
325 330 335
35 Val Arg Arg Glu Ala Arg His His Leu Ala Phe Gly Tyr Gly Val His
340 345 350
Gln Cys Leu Gly Gln Asn Leu Ala Arg Leu Glu Leu Glu Val Ile Leu
355 360 365
40 Thr Ala Leu Phe Glu Arg Leu Pro Gly Leu Arg Leu Ala Val Pro Val
370 375 380
Asp Arg Leu Thr Leu Arg Pro Gly Thr Thr Ile Gln Gly Val Asn Glu
385 390 395 400
Leu Pro Val Thr Trp
405

<210> 6
<211> 63
<212> PRT
<213> Streptomyces sp.TM-7

<400> 6
Met Arg Val Thr Ala Asp Arg Glu Val Cys Val Gly Ala Gly Leu Cys
1 5 10 15
Ala Leu Thr Ala Pro Glu Val Phe Asp Gln Asp Asp Asp Gly Val Val
20 25 30
55 Thr Val Leu Ala Ala Glu Pro Gly Glu Ala Gly Arg Ala Ala Ala Leu
35 40 45

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Glu Ala Gly Val Leu Cys Pro Ser Gly Ala Val Arg Val Val Glu
50 55 60

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<210> 7
<211> 45
<212> DNA
<213> Artificial Sequence

10

<220>
<223> Description of Artificial Sequence:FDR1-1F Primer

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<400> 7
gccatatgac tagtgcgccct cacagactgg aacgggaatc tcatg 45

20

<210> 8
<211> 38
<212> DNA
<213> Artificial Sequence

25

<220>
<223> Description of Artificial Sequence:FDR1-2R Primer
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30

<210> 9
<211> 1438
<212> DNA
<213> Streptomyces coelicolor A3(2)

35

<220>
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<222> (117)..(1376)

40

<400> 9
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gaaggatgac cggaccactc ggtccgtgtg cgcctcacag actggaacgg gaatct atg 119
Met 1

45

ccg cgt gcg aag acg ttc gtg atc gtc ggg ggc ggc ctg gcc gcc ggc 167
Pro Arg Ala Lys Thr Phe Val Ile Val Gly Gly Gly Leu Ala Ala Gly
5 10 15

50

aag gcc gcg gag gaa ctg cgc gag cac ggc cac gac ggg ccg ctt ctc 215
Lys Ala Ala Glu Glu Leu Arg Glu His Gly His Asp Gly Pro Leu Leu
20 25 30

gtg atc ggg gac gag cgg gaa cga ccg tac atc cgg ccg ccg ctg tcc 263
Val Ile Gly Asp Glu Arg Glu Arg Pro Tyr Ile Arg Pro Pro Leu Ser
35 40 45

55

aag ggg tac ctg ctg ggc aag gag gac cgc gag tcc atc cac gtg cac 311
Lys Gly Tyr Leu Leu Gly Lys Glu Asp Arg Glu Ser Ile His Val His
50 55 60 65

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	ccc gag agc tgg tac cgg gag cac gac gtc gat ctg ctc ctc ggc acg	359
	Pro Glu Ser Trp Tyr Arg Glu His Asp Val Asp Leu Leu Leu Gly Thr	
	70 75 80	
5	agc gtg acg tcc gtc gac gcg cgt ggc cgg gcg gtg acg ctg gac gac	407
	Ser Val Thr Ser Val Asp Ala Arg Gly Arg Ala Val Thr Leu Asp Asp	
	85 90 95	
10	ggc cgt cgc gtg ccc tac gcc ggt ctg ctg ctg gcc acc ggt tcc tcc	455
	Gly Arg Arg Val Pro Tyr Ala Gly Leu Leu Leu Ala Thr Gly Ser Ser	
	100 105 110	
	ccg cgc cgc ctg tcc gtg ccg ggc gcg gac ctg gag ggc gtg ctg tac	503
	Pro Arg Arg Leu Ser Val Pro Gly Ala Asp Leu Glu Gly Val Leu Tyr	
	115 120 125	
15	ctg cgg cgc gtg ggc gac agc gag cgc ctc aag gag gcg ttc acc gaa	551
	Leu Arg Arg Val Gly Asp Ser Glu Arg Leu Lys Glu Ala Phe Thr Glu	
	130 135 140 145	
20	gga gcc cgg atc gtg gtg gtc ggc ggc ggc tgg atc ggg ctg gag acg	599
	Gly Ala Arg Ile Val Val Val Gly Gly Gly Trp Ile Gly Leu Glu Thr	
	150 155 160	
	gcg gcg gcg gcc cgg gcg gcc ggc gcg gag gtg acc gtg ctg gag cgc	647
	Ala Ala Ala Ala Arg Ala Ala Gly Ala Glu Val Thr Val Leu Glu Arg	
25	165 170 175	
	ggt gag ctg ccc ctg ctg aag gtc ctg ggc cgc gag gcg gcc gag gtc	695
	Gly Glu Leu Pro Leu Leu Lys Val Leu Gly Arg Glu Ala Ala Glu Val	
	180 185 190	
30	ttc gcc ggt ctg cac cgg gac cac ggt gtg gac ctg cgt ccc cat gcc	743
	Phe Ala Gly Leu His Arg Asp His Gly Val Asp Leu Arg Pro His Ala	
	195 200 205	
	cgg atc gag gcc gtc acc ggc acc ggg ggc cgc gtc gac ggg gtc cgg	791
	Arg Ile Glu Ala Val Thr Gly Thr Gly Gly Arg Val Asp Gly Val Arg	
35	210 215 220 225	
	ctc gcc gac ggc acc cac ctg ccc gcg gac gcc gtg gtc gtg ggg gtg	839
	Leu Ala Asp Gly Thr His Leu Pro Ala Asp Ala Val Val Val Gly Val	
	230 235 240	
40	ggc atc acg ccc aac gtc cgc ctg gcc gag gag gcg ggc ctc gac gtg	887
	Gly Ile Thr Pro Asn Val Arg Leu Ala Glu Glu Ala Gly Leu Asp Val	
	245 250 255	
	cgc aac ggc atc gtg acg gac gcc cgt ctg cgg acc tcc gcc gcc ggg	935
	Arg Asn Gly Ile Val Thr Asp Ala Arg Leu Arg Thr Ser Ala Ala Gly	
45	260 265 270	
	gtc cac gcc gcc ggt gac gtc gcc aac gcc tac cac ccc cgg ctc ggc	983
	Val His Ala Ala Gly Asp Val Ala Asn Ala Tyr His Pro Arg Leu Gly	
	275 280 285	
50	cgg cac ctg cgc gtg gag cac tgg gcc aac gcg ctg cac cag ccc cgt	1031
	Arg His Leu Arg Val His Trp Ala Asn Ala Leu His Gln Pro Arg	
	290 295 300 305	
55	acc gcc gcg ctg agc atg ctc ggc cag gac gcg gtg tac gac cgg ctg	1079
	Thr Ala Ala Leu Ser Met Leu Gly Gln Asp Ala Val Tyr Asp Arg Leu	
	310 315 320	

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55

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Tyr Leu Arg Arg Val Gly Asp Ser Glu Arg Leu Lys Glu Ala Phe Thr
 130 135 140
 5 Glu Gly Ala Arg Ile Val Val Val Gly Gly Gly Trp Ile Gly Leu Glu
 145 150 155 160
 Thr Ala Ala Ala Ala Arg Ala Ala Gly Ala Glu Val Thr Val Leu Glu
 165 170 175
 10 Arg Gly Glu Leu Pro Leu Leu Lys Val Leu Gly Arg Glu Ala Ala Glu
 180 185 190
 Val Phe Ala Gly Leu His Arg Asp His Gly Val Asp Leu Arg Pro His
 195 200 205
 15 Ala Arg Ile Glu Ala Val Thr Gly Thr Gly Gly Arg Val Asp Gly Val
 210 215 220
 Arg Leu Ala Asp Gly Thr His Leu Pro Ala Asp Ala Val Val Val Gly
 225 230 235 240
 20 Val Gly Ile Thr Pro Asn Val Arg Leu Ala Glu Glu Ala Gly Leu Asp
 245 250 255
 Val Arg Asn Gly Ile Val Thr Asp Ala Arg Leu Arg Thr Ser Ala Ala
 260 265 270
 25 Gly Val His Ala Ala Gly Asp Val Ala Asn Ala Tyr His Pro Arg Leu
 275 280 285
 Gly Arg His Leu Arg Val Glu His Trp Ala Asn Ala Leu His Gln Pro
 290 295 300
 30 Arg Thr Ala Ala Leu Ser Met Leu Gly Gln Asp Ala Val Tyr Asp Arg
 305 310 315 320
 Leu Pro Tyr Phe Tyr Thr Asp Gln Tyr Asp Leu Gly Met Glu Tyr Thr
 325 330 335
 35 Gly Tyr Ala Glu Pro Gly Gly Tyr Asp Arg Val Val Phe Arg Gly Ser
 340 345 350
 Arg Glu Glu Arg Arg Phe Leu Ala Phe Trp Met Ser Gly Asp Arg Val
 355 360 365
 Leu Ala Gly Met Ser Val Asn Leu Trp Asp Val Ile Gly Thr Ile Arg
 370 375 380
 40 Ala Leu Ile Glu Ser Gly Ala Glu Thr Asp Asp Ala Ala Leu Ala Asp
 385 390 395 400
 Pro Ser Val Pro Leu Glu Ser Leu Leu Pro Pro His Ala Arg Pro Thr
 405 410 415
 50 Gly Asp Gln Ala
 420

<210> 11
 <211> 43
 <212> DNA
 <213> Artificial Sequence

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<220>

<223> Description of Artificial Sequence:FDR2-3F Primer

<400> 11

cgactagtga cgaggaggca gacaaatggt cgacgcggat cag

43

<210> 12

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:FDR2-4R Primer

<400> 12

cgggatccga caactatgcg acgaggcttt cgaggg

36

<210> 13

<211> 1319

<212> DNA

<213> Streptomyces coelicolor A3(2)

<220>

<221> CDS

<222> (34)..(1296)

<400> 13

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Val Val Asp Ala Asp Gln Thr
1 5

ttc gtc atc gtc gga ggc ggc ctg gcg ggc gcg aaa gcg gcc gag acg 102
Phe Val Ile Val Gly Gly Gly Leu Ala Gly Ala Lys Ala Ala Glu Thr
10 15 20

ctc cgc acg gag ggc ttc acc ggc cgg gtg atc ctc gtc tgc gac gaa 150
Leu Arg Thr Glu Gly Phe Thr Gly Arg Val Ile Leu Val Cys Asp Glu
25 30 35

cgc gac cac ccc tac gag cgc ccg ccg ctg tcc aag ggc tac ctc ctg 198
Arg Asp His Pro Tyr Glu Arg Pro Pro Leu Ser Lys Gly Tyr Leu Leu
40 45 50 55

ggc aag gag gag cgc gac agc gtc ttc gtg cac gag ccc gcc tgg tac 246
Gly Lys Glu Glu Arg Asp Ser Val Phe Val His Glu Pro Ala Trp Tyr
60 65 70

gcc cgg cac gac atc gag ctg cac ctc ggc cag acc gtc gtc gcg atc 294
Ala Arg His Asp Ile Glu Leu His Leu Gly Gln Thr Val Val Ala Ile
75 80 85

gac cgc gcc gcc aag acc gtc cac tac ggc gac gac ggc acc cac gtc 342
Asp Arg Ala Ala Lys Thr Val His Tyr Gly Asp Asp Gly Thr His Val
90 95 100

agc tac gac aag ctg ctc atc gcg acc ggc gcc gag ccc cgc cgc ctg 390
Ser Tyr Asp Lys Leu Leu Ile Ala Thr Gly Ala Glu Pro Arg Arg Leu
105 110 115

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	gac gtc ccc ggc acc ggc ctc gcg ggc gtc cac cac ctg cgc cgc ctg	438
	Asp Val Pro Gly Thr Gly Leu Ala Gly Val His His Leu Arg Arg Leu	
	120 125 130 135	
5	gcg cac gcc gag cgc ctc aag ggc gtc ctc gcc acc ctc ggc cgg gac	486
	Ala His Ala Glu Arg Leu Lys Gly Val Leu Ala Thr Leu Gly Arg Asp	
	140 145 150	
10	aac gga cac ctg gtg atc gcc ggc gcg ggc tgg atc ggc ctg gag gtc	534
	Asn Gly His Leu Val Ile Ala Gly Ala Gly Trp Ile Gly Leu Glu Val	
	155 160 165	
15	gcg gcc gcg gcc cgc gag tac ggt gcg gag gtc acc gtc atc gag ccc	582
	Ala Ala Ala Ala Arg Glu Tyr Gly Ala Glu Val Thr Val Ile Glu Pro	
	170 175 180	
	gcc ccg acc ccg ctg cac ggc gtc ctc ggt ccc gag ctg ggc gcc gtc	630
	Ala Pro Thr Pro Leu His Gly Val Leu Gly Pro Glu Leu Gly Ala Val	
	185 190 195	
20	ttc gcc gag ctg cac gag tcg cgc ggc gtc cgc ttc cgc ttc ggc gtg	678
	Phe Ala Glu Leu His Glu Ser Arg Gly Val Arg Phe Arg Phe Gly Val	
	200 205 210 215	
25	aag ctg acc gag atc gtc ggc cag gac ggt gtg gtg ctg gcc gcc cgc	726
	Lys Leu Thr Glu Ile Val Gly Gln Asp Gly Val Val Leu Ala Ala Arg	
	220 225 230	
	acc gac gac ggc gag gag cac ccc gcg cac gac gtg ctc gcc gcg atc	774
	Thr Asp Asp Gly Glu Glu His Pro Ala His Asp Val Leu Ala Ala Ile	
	235 240 245	
30	ggc gcc gcc ccg cgc acc gcg ctc gcc cag gcg gcc ggg ttg gag atc	822
	Gly Ala Ala Pro Arg Thr Ala Leu Ala Gln Ala Ala Gly Leu Glu Ile	
	250 255 260	
35	gcc gac cgc gcg cac ggc ggc ggc atc gtc gtc gac gac cac ctg cgc	870
	Ala Asp Arg Ala His Gly Gly Ile Val Val Asp Asp His Leu Arg	
	265 270 275	
	acc tcc gac ccc gac atc ttc gcg gcc ggc gac gtg gcc tcc ttc cac	918
	Thr Ser Asp Pro Asp Ile Phe Ala Ala Gly Asp Val Ala Ser Phe His	
	280 285 290 295	
40	cac gcc ctc ttc gac acc agc ctg cgc gtg gag cac tgg gcc aac gcc	966
	His Ala Leu Phe Asp Thr Ser Leu Arg Val Glu His Trp Ala Asn Ala	
	300 305 310	
45	ctg aac ggc ggt ccg gcc gcc gcc cgc gcg atg ctc ggc agg ggc ctc	1014
	Leu Asn Gly Gly Pro Ala Ala Ala Arg Ala Met Leu Gly Arg Gly Leu	
	315 320 325	
	gcc cac gac cgc gtg ccc tac ttc ttc acc gac cag tac gac ctg ggc	1062
	Ala His Asp Arg Val Pro Tyr Phe Phe Thr Asp Gln Tyr Asp Leu Gly	
	330 335 340	
50	atg gag tac tcc ggc tgg gcg ccg gcc ggc tcg tac gac cag gtg gtg	1110
	Met Glu Tyr Ser Gly Trp Ala Pro Ala Gly Ser Tyr Asp Gln Val Val	
	345 350 355	
55	atc cgc ggc gac gcg gcg aag cgc gag ttc atc gcc ttc tgg gtg aag	1158
	Ile Arg Gly Asp Ala Ala Lys Arg Glu Phe Ile Ala Phe Trp Val Lys	
	360 365 370 375	

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5 gag ggc cgg gtg ctg gcc ggg atg aac gtc aac gtg tgg gac gtc acg 1206
 Glu Gly Arg Val Leu Ala Gly Met Asn Val Asn Val Trp Asp Val Thr
 380 385 390

gag ccg atc cag cag ctg atc cgc tgc aag acc cgg gtg gac acg gag 1254
 Glu Pro Ile Gln Gln Leu Ile Arg Ser Lys Thr Arg Val Asp Thr Glu
 395 400 405

10 gac ctg gcg aac ccg cac gta tcc ctc gaa agc ctc gtc gca 1296
 Asp Leu Ala Asn Pro His Val Ser Leu Glu Ser Leu Val Ala
 410 415 420

tagttgtcgg tccgcccccg tag 1319

15 <210> 14
 <211> 421
 <212> PRT
 <213> Streptomyces coelicolor A3(2)

20 <400> 14
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 1 5 10 15

25 Gly Ala Lys Ala Ala Glu Thr Leu Arg Thr Glu Gly Phe Thr Gly Arg
 20 25 30

Val Ile Leu Val Cys Asp Glu Arg Asp His Pro Tyr Glu Arg Pro Pro
 35 40 45

30 Leu Ser Lys Gly Tyr Leu Leu Gly Lys Glu Glu Arg Asp Ser Val Phe
 50 55 60

Val His Glu Pro Ala Trp Tyr Ala Arg His Asp Ile Glu Leu His Leu
 65 70 75 80

35 Gly Gln Thr Val Val Ala Ile Asp Arg Ala Ala Lys Thr Val His Tyr
 85 90 95

Gly Asp Asp Gly Thr His Val Ser Tyr Asp Lys Leu Leu Ile Ala Thr
 100 105 110

40 Gly Ala Glu Pro Arg Arg Leu Asp Val Pro Gly Thr Gly Leu Ala Gly
 115 120 125

Val His His Leu Arg Arg Leu Ala His Ala Glu Arg Leu Lys Gly Val
 130 135 140

45 Leu Ala Thr Leu Gly Arg Asp Asn Gly His Leu Val Ile Ala Gly Ala
 145 150 155 160

Gly Trp Ile Gly Leu Glu Val Ala Ala Ala Ala Arg Glu Tyr Gly Ala
 165 170 175

50 Glu Val Thr Val Ile Glu Pro Ala Pro Thr Pro Leu His Gly Val Leu
 180 185 190

Gly Pro Glu Leu Gly Ala Val Phe Ala Glu Leu His Glu Ser Arg Gly
 195 200 205

55 Val Arg Phe Arg Phe Gly Val Lys Leu Thr Glu Ile Val Gly Gln Asp
 210 215 220

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Gly Val Val Leu Ala Ala Arg Thr Asp Asp Gly Glu Glu His Pro Ala
 225 230 235 240
 5 His Asp Val Leu Ala Ala Ile Gly Ala Ala Pro Arg Thr Ala Leu Ala
 245 250 255
 Gln Ala Ala Gly Leu Glu Ile Ala Asp Arg Ala His Gly Gly Gly Ile
 260 265 270
 10 Val Val Asp Asp His Leu Arg Thr Ser Asp Pro Asp Ile Phe Ala Ala
 275 280 285
 Gly Asp Val Ala Ser Phe His His Ala Leu Phe Asp Thr Ser Leu Arg
 290 295 300
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Claims

1. A system for the expression of actinomycete cytochrome P-450 genes in host *Escherichia coli*, wherein said *Escherichia coli* supports a recombinant DNA molecule which comprises xenogenic microorganism-originated ferredoxin gene, ferredoxin reductase gene as well as said cytochrome P-450 gene, in operable state.
2. An expression system of claim 1 wherein ferredoxin gene and ferredoxin reductase gene are independently originated from some strain of actinomycete.
3. An expression system of claim 1 wherein ferredoxin gene is originated from microorganism selected from the group consisting of those belonging to genus *Microtetraspora* and those belonging to genus *Pseudomonas*.
4. An expression system of claim 1 wherein ferredoxin reductase gene is originated from microorganism selected from the group consisting of those belonging to genus *Streptomyces* and those belonging to genus *Pseudomonas*.
5. An expression system of claim 1 wherein actinomycete cytochrome P-450 gene and ferredoxin gene are originated from one and the same gene cluster of actinomycete.
6. An expression system of claim 1 wherein ferredoxin reductase gene is originated from *Streptomyces coelicolor*.

7. An expression system of claim 1 wherein actinomycete cytochrome P-450 gene and ferredoxin gene are originated from one and the same gene cluster of actinomycete, and wherein ferredoxin reductase gene is originated from *Streptomyces coelicolor*.
- 5 8. An expression system of claim 1 wherein ferredoxin gene and ferredoxin reductase gene are respectively putidaredoxin gene (*camB*) and putidaredoxin reductase gene (*camA*) which are each originated from *Pseudomonas putida*.
- 10 9. An expression system of claim 1 in which actinomycete cytochrome P-450 gene and ferredoxin gene are originated from one and the same gene cluster of actinomycete, and which further contains, as another ferredoxin gene, putidaredoxin gene (*camB*) originated from *Pseudomonas putida*.
- 15 10. An expression system of claim 1 in which actinomycete cytochrome P-450 gene and ferredoxin gene are originated from one and the same gene cluster of actinomycete, in which ferredoxin reductase gene is putidaredoxin reductase gene (*camA*) originated from *Pseudomonas putida*, and which further contains, as another ferredoxin gene, putidaredoxin gene (*camB*) originated from *Pseudomonas putida*.
- 20 11. An expression system of claim 1 wherein actinomycete cytochrome P-450 gene and ferredoxin gene are respectively compactin-hydroxylating enzyme-encoding gene (*moxA*) originated from *Microtetraspora recticattina* and ferredoxin gene (*moxB*) which is adjacent downstream to *moxA*.
- 25 12. An expression system of claim 1 wherein actinomycete cytochrome P-450 gene and ferredoxin gene are respectively compactin-hydroxylating enzyme-encoding gene (*moxA*) originated from *Microtetraspora recticattina* and ferredoxin gene (*moxB*) which is adjacent downstream to *moxA*, and wherein ferredoxin reductase gene is ferredoxin reductase gene *fdr-1* or *fdr-2* originated from *Streptomyces coelicolor*.
- 30 13. An expression system of claim 1 in which actinomycete cytochrome P-450 gene and ferredoxin gene are respectively compactin-hydroxylating enzyme-encoding gene (*moxA*) originated from *Microtetraspora recticattina* and ferredoxin gene (*moxB*) adjacent downstream to *moxA*, and which further contains, as another ferredoxin gene, putidaredoxin gene (*camB*) originated from *Pseudomonas putida*, and in which ferredoxin reductase gene is putidaredoxin reductase gene (*camA*) originated from *Pseudomonas putida*.
- 35 14. An expression system of claim 1 in which the induction of expression of cytochrome P-450 gene is conveniently carried out at 20 to 24°C.
- 40 15. An expression system of claim 1 wherein said cytochrome P-450 gene comprises polynucleotide which is selected from the group consisting of polynucleotide having a continuous nucleotide sequence from base 313 to base 1533 in Sequence No. 1 or functionally equivalent polynucleotide with homology of at least 80 % to said nucleotide sequence, and polynucleotide having a continuous nucleotide sequence from base 544 to base 1758 in Sequence No. 2 or functionally equivalent polynucleotide with homology of at least 80 % to said nucleotide sequence.
- 45 16. An expression system of claim 1 wherein said ferredoxin gene comprises polynucleotide which is selected from the group consisting of polynucleotide having a continuous nucleotide sequence from base 1547 to base 1741 in Sequence No. 1 or functionally equivalent polynucleotide with homology of at least 80 % to said nucleotide sequence, and polynucleotide having a continuous nucleotide sequence from base 1782 to base 1970 in Sequence No. 2 or functionally equivalent polynucleotide with homology of at least 80 % to said nucleotide sequence.
- 50 17. An expression system of claim 1 wherein said ferredoxin reductase gene comprises polynucleotide which is selected from the group consisting of polynucleotide having a continuous nucleotide sequence from base 118 to base 1377 in Sequence No. 5 or functionally equivalent polynucleotide with homology of at least 80 % to said nucleotide sequence, and polynucleotide having a continuous nucleotide sequence from base 34 to base 1296 in Sequence No. 8 or functionally equivalent polynucleotide with homology of at least 80 % to said nucleotide sequence.
- 55 18. An expression system of claim 1 wherein said ferredoxin gene comprises polynucleotide having a continuous nucleotide sequence from base 1439 to base 1759 in Sequence No. 16 or functionally equivalent polynucleotide with homology of at least 80 % to said nucleotide sequence.
19. An expression system of claim 1 wherein said ferredoxin reductase gene comprises polynucleotide having a con-

tinuous nucleotide sequence from base 115 to base 1380 in Sequence No. 16 or functionally equivalent polynucleotide with homology of at least 80 % to said nucleotide sequence.

- 5 **20.** A method to introduce a hydroxyl group at 6 β -position of compactin with use of the expression system of claim 12 or 13.

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Fig. 1

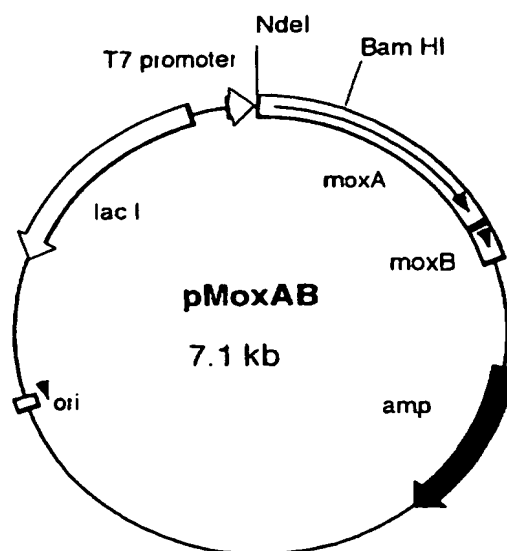


Fig. 2

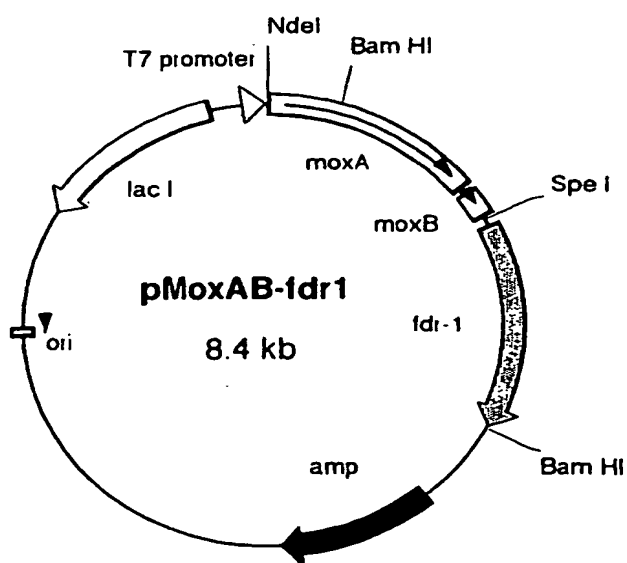


Fig. 3

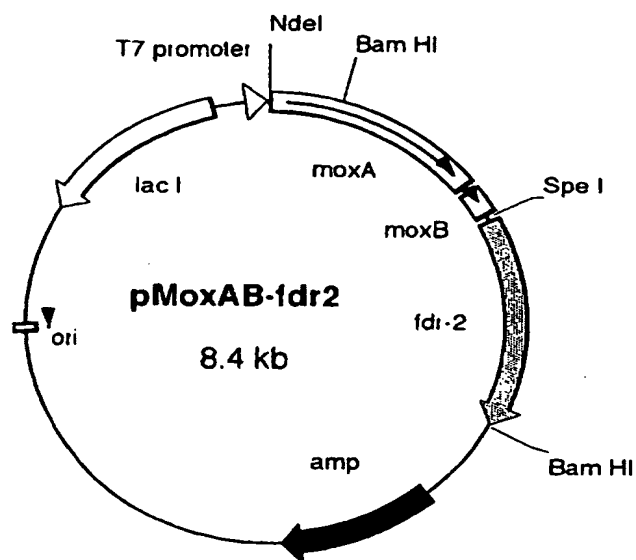


Fig. 4

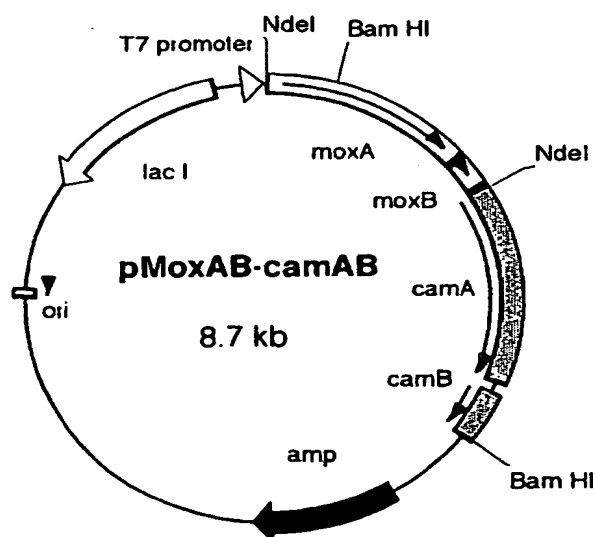


Fig. 5

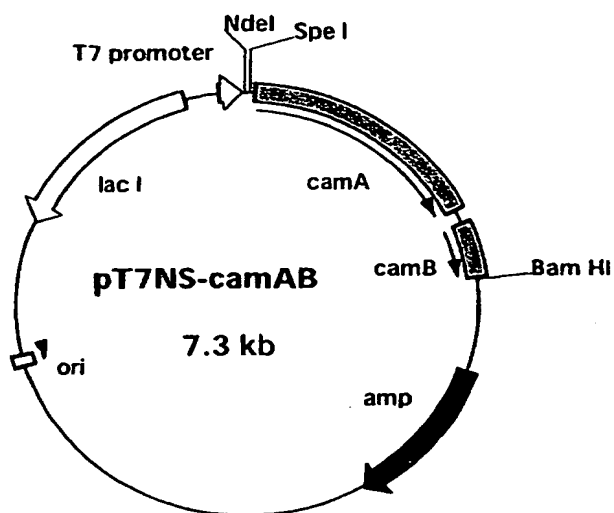


Fig. 6

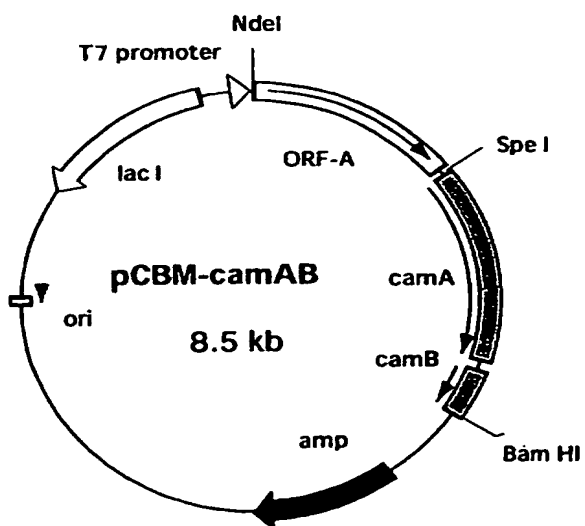


Fig. 7

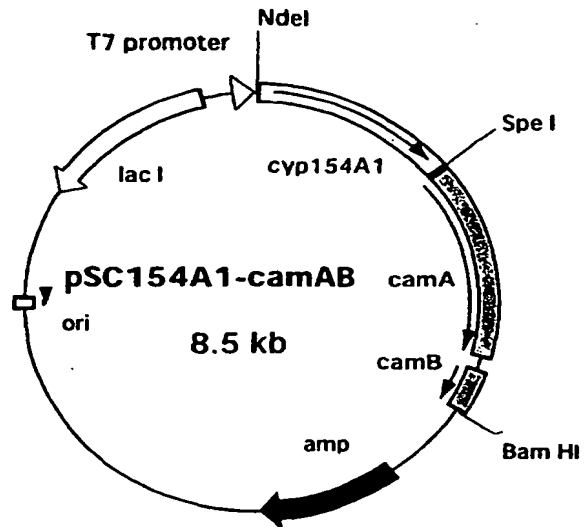
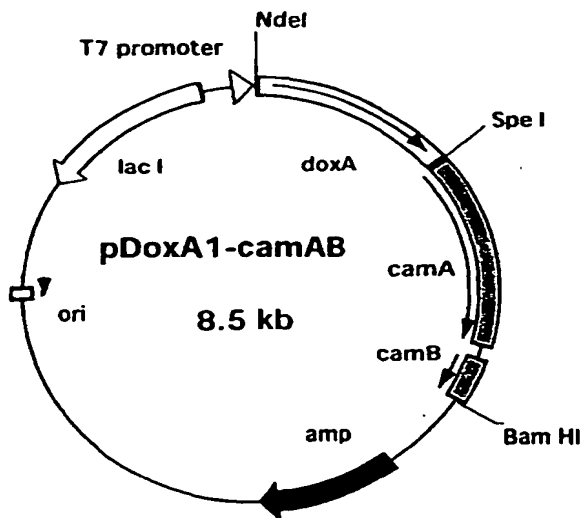


Fig. 8



INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP03/04609

A. CLASSIFICATION OF SUBJECT MATTER

Int.Cl⁷ C12N15/70, C12N15/53, C12N15/12, C12P7/62 // C12N15/53,
C12N1/21, (C12N15/70, C12R1:04), (C12N15/53, C12R1:38),
(C12N15/12, C12R1:465), (C12N15/12, C12R1:38),

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

Int.Cl⁷ C12N15/00-90, C12P1/00-41/00, C12N1/00-38, C12N9/00-99

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

MEDLINE (STN), WPI (DIALOG), BIOSIS (DIALOG), GenBank/EMBL/DBJ/GeneSeq,
SwissProt/PIR/GeneSeq

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y A	JP 07-067666 A (Sumitomo Chemical Co., Ltd.), 14 March, 1995 (14.03.95), & EP 477961 A1 & US 5668000 A	1-10, 14 11-13, 15-20
Y A	WO 93/12236 A1 (E.I. DU PONT DE NEMOURS & CO.), 24 June, 1993 (24.06.93), & JP 07-502650 A & EP 618972 A1 & US 5466590 A	1-10, 14 11-13, 15-20
Y	Peterson J.A. et al., "Putidaredoxin reductase and putidaredoxin. Cloning, sequence determination, and heterologous expression of the proteins.", J.Biol.Chem.(1990), Vol.265, No.11, pages 6066 to 6073	3, 4, 8-10

☒ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents: "A" document defining the general state of the art which is not considered to be of particular relevance "E" earlier document but published on or after the international filing date "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) "O" document referring to an oral disclosure, use, exhibition or other means "P" document published prior to the international filing date but later than the priority date claimed	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art "&" document member of the same patent family
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Date of the actual completion of the international search
06 May, 2003 (06.05.03)

Date of mailing of the international search report
27 May, 2003 (27.05.03)

Name and mailing address of the ISA/
Japanese Patent Office

Authorized officer

Facsimile No.

Telephone No.

Form PCT/ISA/210 (second sheet) (July 1998)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP03/04609

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 97/19917 A1 (L'OREAL SA), 05 June, 1997 (05.06.97), & JP 10-504845 A & EP 805800 A1 & US 6278001 B1	20

Form PCT/ISA/210 (continuation of second sheet) (July 1998)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP03/04609

Continuation of A. CLASSIFICATION OF SUBJECT MATTER
(International Patent Classification (IPC))

Int.Cl⁷ (C12P7/62, C12R1:19), (C12N1/21, C12R1:19)

(According to International Patent Classification (IPC) or to both
national classification and IPC)